Australian Journal of Biomedical Research
(eISSN 3083-4708)

Editorial Article

Advancing Knowledge, Fostering Collaboration: Welcome to the Australian Journal of Biomedical Research

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Received: Aug 18, 2025
Accepted: Aug 18, 2025

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It is with a great pleasure that I introduce the inaugural issue of the Australian Journal of Biomedical Research. This marks the beginning of both a new chapter for the journal and my tenure as Editor-in-Chief. I take this role with enthusiasm and humility, committed to ensuring that the journal fulfills its mission of publishing high quality, innovative research that advances knowledge across the field of biomedical sciences.

The establishment of this journal has been made possible through the dedication and support of many colleagues, to whom I am deeply grateful. I am privileged to work alongside an exceptional team of Associate Editors and Board members whose expertise spans a wide range of disciplines and whose contributions represent the forefront of biomedical research worldwide. Together, we aim to foster a platform that reflects both the interdisciplinary nature of modern science and the international collaboration that drives it forward.

The launch of the Australian Journal of Biomedical Research comes at a time when scientific and medical publishing faces unprecedented challenges. The rapid growth of open-access models has expanded access to knowledge, yet it has also raised questions about sustainability, equity, and affordability, particularly for researchers in resource-limited settings. The increasing volume of submissions highlights the ongoing need to preserve the integrity of peer review, which is essential for maintaining trust in scholarly communication. Moreover, technological innovations, including AI-assisted writing and the expansion of preprint servers, further complicate the landscape by reshaping how knowledge is created, disseminated, and evaluated. These developments highlight some of the challenges ahead and the critical role of scientific and medical journals in maintaining both quality and trust in scholarly communication.

Thus, the Australian Journal of Biomedical Research is founded on principles that directly address these challenges. Our publishing model emphasizes on accessibility while ensuring financial sustainability, lowering barriers for authors and readers globally. We are committed to rigorous and transparent peer review process, upholding the highest standards of editorial integrity. We will embrace technological innovation responsibly, ensuring that digital advances are used to enhance, rather than compromise, the quality of scientific communication.

The Australian Journal of Biomedical Research will actively promote open science practices, encourage robust methodological reporting, and support data sharing initiatives. This journal seeks to provide a platform for interdisciplinary biomedical research and to contribute meaningfully to building a more transparent, equitable, and trustworthy future for scholarly publishing.

I welcome our readers, authors, and reviewers to join us in this endeavor. Together, we can ensure that the Australian Journal of Biomedical Research becomes a leading forum for advancing knowledge, fostering collaboration, and shaping the future of biomedical science.

Australian Journal of Biomedical Research
(eISSN 3083-4708)

Review Article

Pharmacogenomics Applications in Clinical Practice: Revolutionizing Patient Care

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Received: July 29, 2025
Accepted: Aug 09, 2025

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Abstract:

Background: Personalised medicine through pharmacogenomics is revolutionalizing healthcare delivery by encouraging individualized therapy that takes into consideration an individual's genetic profile, environment and lifestyle. Pharmacogenomics is an aspect of pharmacy that studies the relationship between genetic profile and response to therapeutic agents. However, the application of the concepts of pharmacogenomics in healthcare helps in achieving more effective and safe responses from therapy. This study evaluates the application and benefits of pharmacogenomics in clinical practice based on evidence from current practices in various medical fields.

Methods: In carrying out this review, PubMed database was the primary literature source and we analyzed and synthesized findings from the included literature thematically as it relates to pharmacogenomics applications, benefits and challenges as well as safety and ethical concerns.

Results: Pharmacogenomics has been widely applied in various aspects of healthcare such as in dosing, choice of treatment, reducing and management of adverse reactions, individualization of therapy, optimizing efficacy of therapy. Despite its numerous applications, its adoption faces challenges such as limited clinical evidence, lack of specialized training among healthcare professionals, cost and complexity of genetic mapping as well as ethical concerns.

Conclusion: With ongoing advances in genomic technologies, pharmacogenomics is becoming an integral aspect of individualization therapy in clinical practice and more widely applied in different healthcare sectors.

Keywords: Pharmacogenomic; Clinical practice; Personalized medicine; Gene testing; Precision medicine.

Introduction

Personalised medicine is an evolutionary approach in healthcare that takes into account an individual's genetic makeup, lifestyle, and environment in tackling healthcare related needs of patients such as therapeutic management, optimizing therapeutic outcomes as well as improving or maintaining quality of life [1]. On the other hand, pharmacogenomics, which is the cornerstone of personalized medicine, has to do with the study of an individual's response to treatment regimen in relation to the person's genetic profile. It features studies on drug interaction, gene structure and function at a molecular level for application in drug development [2].

Understanding how genetic factors influence drug absorption, distribution, metabolism, and excretion enables healthcare professionals to determine individuals who may benefit from a medication and those who may experience Adverse Drug Reactions (ADRs). Patients exhibit variable response to prescribed medication, this highlights the significance of personalized medicine in healthcare. For example, some drugs are highly effective in certain patients, but others do not experience the same effectiveness. Instead, they are faced with debilitating ADRs from the same drugs. These variations in responses majorly arise from significant differences in genetic makeup of individuals [3].

In the past decade, several studies on pharmacogenomics have uncovered the genetic variations that influence differences in drug response. Advances in genomic technology such as next-generation sequencing and microarray-based comparative genomic hybridization have played a key role in enabling the Integration of pharmacogenomics into medical practice by making genetic testing more accessible and affordable [4]

Moreover, platforms like the Clinical Pharmacogenetics Implementation Consortium (CPIC) and the Pharmacogenomics Knowledge Base (PharmGKB) have encouraged the clinical practice of pharmacogenomics by providing guidelines that allow clinicians to apply pharmacogenomics in healthcare settings [5]. However, several challenging factors limit the full implementation of pharmacogenomics in clinical practice some of which include insufficient clinical evidence, inadequate education of healthcare providers in pharmacogenomics, as well as lack of equipment and infrastructure for genomic testing and data storage. Nevertheless, the application of pharmacogenomics in personalized medicine not only holds the potential for more effective treatment, but promises to minimize ADRs encountered by patients leading to cost-effective healthcare [6].

Nevertheless, in carrying out this review, it was hypothesized that the application of pharmacogenomics in clinical practice will significantly improve patient outcomes. However, this review aims to synthesize evidence supporting the applications of pharmacogenomics in clinical practice, as well as explore the benefits of such application and challenges hindering application.

Ultimately, this paper is essential for healthcare professionals, as it provides a comprehensive overview of applications of pharmacogenomics in clinical practice and its potential to improve clinical outcomes and guide decision-making. By addressing the barriers to its implementation, the study aims to guide clinicians in adopting pharmacogenomics.

The Science of Pharmacogenomics

Pharmacogenomic studies are based on the understanding of the basic principles of drug responses in a biological system, which is essentially the pharmacokinetics and pharmacodynamics of the drug. The combination of this understanding with the knowledge of genetic differences that lead to varying phenotypes provides insight on what drugs will be safe and effective for certain kinds of people and at what dose [7]. Pharmacokinetics describes the body's interaction with administered drugs, encompassing factors such as absorption, distribution, metabolism, and excretion, while pharmacodynamics describes factors that affect the drug's action on the target protein, including receptors, intracellular enzymes, and cell membrane channels [8].

The genetic involvement in the pharmacokinetics and pharmacodynamics can be explained with the evaluation of one of the most studied families of enzymes driving drug metabolism (cytochrome P450). Cytochrome P450 genes such as CYP2C9, CYP2C19, and CYP2D6 can be produced from varying DNA nitrogenous base sequences. Varying cytochrome P450 enzymes with differences in amounts, degree of enzymatic activity, and therefore varying abilities to metabolize drugs are subsequently produced from these gene variants. As a consequence,

individuals with certain variants of cytochrome P450 enzymes may metabolize drugs more slowly or more rapidly, impacting efficacy and the risk of side effects [9, 10, 11].

Furthermore, the majority of the genes coding for ATP-binding cassette transporters, which facilitate movement of several drugs through cells, exist in many different versions (alleles) within populations, contributing to variations in how well the proteins transport drugs and hence biological responses, which may be to increasing or decreasing degrees [12] [13]. These variations impact the effectiveness of the drugs and the risk of serious adverse events.

The impact of genetic variations on drug response is evident in the diverse areas of therapy. In oncology, the efficacy and safety of thiopurine drugs used in the treatment of leukaemia are influenced by the genetic variation of the thiopurine S-methyltransferase (TPMT) gene encoding for the TPMT enzyme required for the metabolism of thiopurine drugs [14, 15]. These variations may lead to adverse drug reactions in certain patients, necessitating dose adjustments based on genetic testing. In cardiology, the effectiveness of clopidogrel in patients with acute myocardial events is impacted by its conversion to an active metabolite by cytochrome P450 2C19 (CYP2C19) enzyme. The presence of two copies of the CYP2C19 gene in an individual leads to poor enzymatic activity and an inability to benefit from the antiplatelet function of the drug [16]. However, in psychiatry, genetic polymorphisms of CYP2C19 and CYP2D6 enzymes used in phase 1 metabolism of most antidepressants and antipsychotics, and genetic variations in neurotransmitter receptors contribute to suboptimal drug exposure and minimal tolerability of these drugs, necessitating prescriber reliance on pharmacogenomics drug label recommendations [17, 18].

Application of Pharmacogenomics in Clinical Practice

Incorporation of pharmacogenomics in clinical practice has significantly transformed disease treatment and prevention in diverse therapeutic areas. In cardiology, clopidogrel has been widely used as antiplatelet, however, considerable concern has been raised due to the significant variability in response to the P2Y12 receptor antagonist, largely dependent on the presence of the CYP2C19 gene variant [19]. According to Cavallari & Pratt, (2022) [20], CYP2C19 testing in line with pharmacogenomics concept can help predict patients unlikely to have maximum benefit from clopidogrel in whom alternative therapy may be initiated [20].

Additionally, understanding which Vitamin K Epoxide Reductase Complex subunit 1 gene (VKORC1) and CYP2C9 alleles are possessed by a patient informs personalized warfarin dosing during the stabilization phase of anticoagulant therapy [21]. In oncology, personalized cancer therapy can be achieved through genetic profiling of tumors, enabling the selection of targeted therapies that are more effective and have fewer side effects [22]. Classification of human epidermal growth factor receptor 2 (HER2) protein expressions through pharmacogenomics has informed targeted therapy using Trastuzumab, a monoclonal antibody in the treatment of breast cancers [23].

In neuropsychiatry, personalized treatment using different antidepressants and antipsychotics can be achieved by the application of pharmacogenomics in the classification of patients as poor metabolizers, intermediate metabolizers, normal metabolizers, and rapid or ultrarapid metabolizers based on the expression of cytochrome P450 variants responsible for metabolism, leading to the selection of therapy with maximum efficacy and minimum toxicity [24]. Moreover epileptic medications such as carbamazepine require Human Leukocyte Antigen B1502 (HLA-B1502) testing to prevent life-threatening skin diseases like Stevens-Johnson syndrome in positive individuals [25].

In infectious diseases therapy, pharmacogenomics guides the selection of antiviral and antimicrobial therapy by determining genetic variants related to disease susceptibility and response to antimicrobial therapy [26]. For example, in the management of HIV, Human Leukocyte Antigen B5701 (HLA-B5701) allele testing is conducted to determine the presence of HLA-B*57:01 before administering Abacavir to patients so as to prevent hypersensitivity reactions in positive alleles [27].

Table 1 summarizes various drugs and the relevant genetic tests that guide their application in clinical practice in line with pharmacogenomic principles.

Table 1: Some genetic tests required in the application of pharmacogenomics in clinical practice

Condition	Drug	Gene Tested	Impact of Gene
HIV Management	Abacavir	HLA-B5701	High risk of hypersensitivity reaction in positive allele
Epilepsy/Neuropathic pain	Carbamazepine	HLA-B1502	Increased risk of severe skin reactions in certain populations
Antiplatelet Therapy	Clopidogrel	HLA-B1502	Variants affect drug activation and risk of stent thrombosis
Breast Cancer	Trastuzumab/T-DM1	HER2/NEU	Ensures efficacy for HER2-positive breast cancer patients
Breast Cancer	Tamoxifen	CYP2D6	Poor metabolizers may need alternative therapies or doses
Pain Relief	Codeine	CYP2D6	Poor or ultra-rapid metabolizers affect drug efficacy
Anticoagulant	Warfarin	CYP2C9, VKORC1	Guides dose adjustment to prevent bleeding or clotting
Chemotherapy	Irinotecan	UGT1A1 (UDP Glucuronosyltransferase 1A1)	Influences dosing to avoid severe side effects
Immunosuppression	Azathioprine/6-mercaptopurine	TPMT	Increases risk of severe toxicity
Colorectal Cancer	Cetuximab/Panitumumab	KRAS (Kirsten Rat Sarcoma Viral Oncogene Homolog)	Mutation status determines drug efficacy in colorectal cancer

Benefits and Challenges

Pharmacogenomics holds benefits capable of transforming healthcare approaches and enhancing treatment outcomes. However, the application of pharmacogenomics is accompanied by a number of challenges.

Potential benefits of pharmacogenomics in healthcare

I. Reduced Adverse Drug Reactions

One of the most significant benefits of pharmacogenomics is that it reduces incidences of adverse drug reactions (ADRs). ADRs have diverse implications for the health of individuals worldwide, some of which may be life threatening, largely resulting from a one-drug-fits-all approach or polypharmacy. Diverse genes influence an individual's response (negative or positive) to a drug. By understanding the genetic variants possessed by a patient and how they influence drug response, treatment can be initiated with interventions that do not elicit negative responses [28]. This impacts on health outcomes by ensuring that drugs are safe and only positive responses are obtained from a drug.

For example, Pharmacogenomic testing for abacavir and carbamazepine has prevented significant adverse drug reactions (ADRs) that could have been life threatening. Genetic testing before initiating carbamazepine and abacavir therapies helps to identify at-risk patients, allowing clinicians to prescribe safer options and avert fatal side effects. The extensive use of pharmacogenomic testing for these medications has reduced ADR hospitalizations, healthcare costs, and promoted patient safety and outcomes from therapy.

II. More Efficacious Drugs

Pharmacogenomics impacts informed research and drug development tailored to specific genes associated with effective responses and their encoded proteins, enzymes, and RNA molecules. Discovery of therapy can then be supported by findings from genetic testing, leading to the development of drugs that target specific diseases [29]. With this approach pharmaceutical

companies are able to synthesize therapeutic substances that are more potent.

For example, Pharmacogenomic testing for trastuzumab, T-DM1, and irinotecan has improved cancer treatment outcomes by ensuring patients receive the most effective medications. Trastuzumab and T-DM1 are targeted therapy for HER2-positive breast cancer (with overexpressed Human Epidermal Growth Factor Receptor 2 (HER2/NEU) gene). Testing for HER2/NEU expression helps to evaluate if these medications are right for a patient, ensuring that only those who will benefit from it receive the therapy. This targeted and personalized treatment approach helps to improve survival rates and reduce healthcare costs [30, 31].

III. Increased Accuracy in Dosage Determination

Pharmacogenomics provides a more accurate method of dosage determination. Personalising drug dosage based on the individual's unique genetic profile instead of age or weight will ensure more accuracy [32, 33]. This will ensure that maximum value is obtained from the therapy and reduce the likelihood of underdose or overdose.

For example, CYP2C9 and VKORC1 genetic variants alter warfarin metabolization, affecting efficacy and risk of bleeding or clotting. Before administering warfarin, doctors can carry out genetic testing to evaluate the patient's genetic profile to ensure proper dosage. Haemorrhages, which require expensive medical procedures, blood transfusions, and longer hospital stays, can be avoided with precise dosing. Therefore, pharmacogenomic testing helps to reduce healthcare costs by eliminating the trial-and-error approach to warfarin dosing [34, 35].

IV. Overall Reduction in Cost of Healthcare

Applying pharmacogenomics potentially leads to a reduction in the financial burden of healthcare by decreasing the occurrence of adverse drug reactions, minimizing patients' duration of therapy, decreasing the number of medications that have to be prescribed in the trial-and-error method, and increasing the number of effective drugs produced by pharmaceutical companies [36]. Figure 1 below summarizes the benefits of applying pharmacogenomics in healthcare.

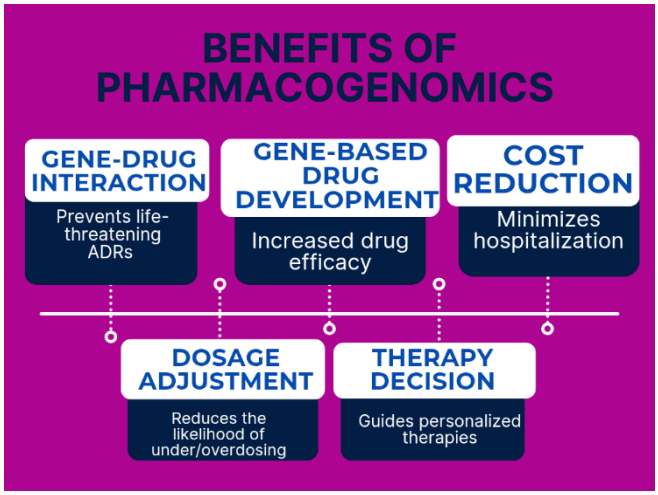

Figure 1: Benefits of Pharmacogenomics in Clinical Practice

Challenges and limitations of implementing pharmacogenomics

The challenges that have to be overcome before pharmacogenomics can be fully adopted include:

I. Minimum evidence from large-scale studies

Though data from clinical studies exist which serve as evidence to support the application of pharmacogenomics in some areas of therapy such as psychiatry and cardiology, there is limited research data to support its application of therapy in other therapeutic areas [37]. This lack of strong clinical evidence makes it difficult for pharmacogenomics to be applied in routine healthcare.

II. Cost and complexity of genetic testing

The cost and complexity of genetic testing significantly impact the seamless adoption of pharmacogenomics. Though the cost of genomic sequencing has reduced considerably in high-income countries, low- and middle-income countries still face severe financial constraints limiting the adoption of pharmacogenomics in these areas [38]. Moreover, genetic testing is a complex process, and the results may not be available until after several hours or even days, after which the patient would have to be contacted before therapy is initiated or not [38].

III. Policy regulation and ethical issues

The implementation of pharmacogenomics requires regulatory guidelines that define the use of genetic profile data. Genetic information is highly confidential; therefore, large-scale collection of genetic information and clinical data raises privacy issues since this information can be put to the wrong use. Policy that establishes ethical use of genetic data is largely lacking [39].

IV. Inadequate training of healthcare professionals

Inadequate training and education of healthcare professionals in pharmacogenomics has become a hindrance to its execution, especially in low- and middle-income countries [40]. Low- and middle-income areas like Africa are lacking in healthcare professionals, most of whom lack specialty training, making education in pharmacogenomics even more challenging.

Ethical and Societal Implications

Ethical Considerations in Pharmacogenomics

The use of genetic information in healthcare is accompanied by several ethical concerns. One of these concerns is the social discrimination that may be encountered by some people due to their genetic predisposition [41]. Though developed countries like the United States have instituted a legislative framework like the Genetic Information Nondiscrimination Act (GINA) to protect individuals from such discrimination, many other countries do not have such established legislation [42]. Another concern is the need for privacy and confidentiality. Genetic information is deeply personal and may be accessed by unauthorized individuals if not properly protected, leading to misuse [40]. A major ethical issue is informed consent. Before genetic testing is conducted, individuals should be made to fully understand what they are agreeing to, including the nature of data being collected, how it would be used, and the possible implications, including incidental findings like susceptibility to unrelated genetic conditions [43]. Finally, data protection is an issue as digitalization of healthcare may increase unauthorized access to genetic information leading to identity theft and misuse [41].

Potential implications for patients, healthcare professionals, and society

Pharmacogenomics is a revolutionary approach that has a wide range of implications for individuals at different levels. For patients, it promises to offer more effective and safer treatment strategies to ensure improved health outcomes. However, despite the benefits of personalized medicine through pharmacogenomics, the gaps in access to genomic testing due to limited access in developing regions may lead to unequal health outcomes [44].

For healthcare professionals, pharmacogenomics is a new area that is gradually being incorporated into healthcare and requires new skills and competencies. As personalized medicine is becoming the new order of practice, ongoing education and training is necessary for health care professionals to accurately apply genomic testing results to clinical decision-making processes and guide patients accordingly [45].

Universal adoption of pharmacogenomics at the societal level has the potential to transform healthcare delivery, public health intervention and monitoring, as well as drug development [46]. Governing bodies in different regions will also be required to institute policies that ensure adequate data protection and security.

Implementation and Integration

Strategies for Implementing Pharmacogenomics in Clinical Practice

Successfully implementing pharmacogenomics requires a multiple-solution strategy. One of the key strategies is education and training of healthcare professionals [47]. This would enable frontline medical practitioners to understand genetic information and utilize genomic data in clinical decision-making and prescribing; hence, educational institutions should integrate pharmacogenomics into medical curricula to prepare clinicians for its application in practice.

Also, integrating pharmacogenomic testing into Electronic Health Records, along with other smart clinical support tools, can enable clinicians to rapidly and effectively use genetic information in the treatment of patients at the point of care. This strategy is already being implemented by a number of institutions and has demonstrated improved efficiency and clinical outcomes [48].

Another key strategy is developing clear, evidence-based clinical guidelines to enable clinicians to understand and use patients' genetic test results. These guidelines, such as those provided by CPIC and

the Dutch Pharmacogenetics Working Group, would transform complex genetic test results into practical steps guiding clinicians when treating patients [59].

Integrating Pharmacogenomics into Healthcare Systems

For healthcare systems to successfully offer pharmacogenomic services, key infrastructure and policies must be adopted. Healthcare systems must have access to well-equipped laboratories capable of carrying out genetic testing, and establish data-sharing infrastructure like functional computational systems to ensure that different departments of the system, such as laboratory, pharmacy, and clinics, freely access, share, and use genetic data smoothly.

Additionally, policies which ensure genetic tests used are accurate, reliable, and approved by relevant bodies (e.g., Food and Drug Administration (FDA) or local health regulatory bodies), patients' privacy and data protection, as well as ethical guidelines which prevent genetic discrimination and ensure patients give informed consent, must be adopted. Sustainable funding systems are also necessary for the smooth running of genetic testing and pharmacogenomic technologies within healthcare systems.

Collaborations between government (e.g., health ministries or national research institutes) and private groups (e.g., biotech companies, pharmaceutical firms, or healthcare providers) would facilitate the development and improvement of pharmacogenomics tools and also promote the widespread use of these technologies within healthcare institutions.

Furthermore, actively involving patients and the general public through education to enlighten individuals on the implications of pharmacogenomics for their health outcomes, together with advocacy for the use of pharmacogenomics, will help build confidence and enhance acceptance.

Current Status and Future Prospects

Current state of pharmacogenomics and personalized medicine

Advances in pharmacogenomics have increased its recognition as a standard component of contemporary health care. The extensive integration of pharmacogenomics information into the US Food and Drug Administration (FDA)-approved drug labels for over 300 drugs shows that several pharmacogenomics tests identifying drug-gene pairs have been approved by the regulatory body and have been widely accepted in mainstream healthcare [50]. Also, in a bid to strengthen the integration of pharmacogenomics in routine clinical practice and enable clinicians interpret pharmacogenomics data in clinical practice, freely accessible gene/drug regulatory guidelines have been developed by institutions like the Clinical Pharmacogenetics Implementation Consortium (CPIC) [51].

Application of pharmacogenomics in personalised medicine has commenced in major areas of clinical practice like oncology (where targeted cancer treatment is guided by pharmacogenomics testing for HER2, Kirsten rat sarcoma viral oncogene homolog (KRAS), and Epidermal Growth Factor Receptor (EGFR) mutations) [52, 53], psychiatry and cardiology. Additionally, preemptive pharmacogenomics testing is routinely conducted in some healthcare institutions, which involves testing patients for a collection of genes related to drug response and storing the results in their electronic health records. These records are used to predict drug response and alert clinicians when a prescribed drug is unsuitable for a patient [54].

Emerging trends and future directions

One of the latest trends which has emerged in the pharmacogenomics field is the utilisation of artificial intelligence and machine learning in pharmacogenomics studies to aid the analysis of large-scale genomic data, thereby improving the prediction of drug response and treatment outcomes in clinical settings [55]. Pharmacogenomics have been integrated with other powerful biological study approaches like proteomics, metabolomics, and transcriptomics. These omics technologies offer a more comprehensive understanding of the reasons for variation in drug responses among individuals. Combining this data with pharmacogenomics holds promise to enhance drug response prediction in personalised medicine [56].

Also, emerging compact and easy-to-use technological devices like Genedrive® System, ID Now™, and Spartan RX CYP2C19, capable of analyzing specific genes within an hour, and other advances in point-of-care technologies are capable of shifting pharmacogenomics from specialized lab environments to the bedside [57, 58].

Future directions necessary for improved adoption of pharmacogenomics in clinical practice include:

- More robust integration of pharmacogenomics in routine clinical practice.
- Expansion of research to include more gene candidates that are involved in drug response regarding other diseases aside from cardiovascular disease, mental health disorders, and cancer.
- Conducting preemptive testing before illnesses emerge or before treatments commence to ensure that drug choices are immediately available when needed.
- Establishing the use of machine learning and deep learning for the analysis of large genomic data sets to realize more accurate prediction of drug response.
- Developing standardized regulatory guidelines and insurance policies to encourage the adoption of pharmacogenomics in clinical practice.

Conclusion

Evidently, personalised medicine piloted by pharmacogenomics signifies the emergence of a new era in healthcare. Pharmacogenomics facilitates individualisation of drug therapy by harnessing patients' genetic profiles, leading to enhanced efficacy, reduced adverse drug reactions, and improved cost-effectiveness. Though pharmacogenomics comes with numerous benefits for the general population, a number of challenges still hinder its widespread use and implementation in routine clinical practice, including inadequate clinical evidence, high cost of implementation, as well as ethical considerations. To enable the successful integration of pharmacogenomics, these challenges must be strategically addressed.

Judging from the ongoing progress and development in areas such as research, technology, and policy development in the field of pharmacogenomics, it is evident that the future holds great promise of more personalized drug therapy which is safe and effective, providing better health outcomes. As healthcare moves towards personalized medicine, collaboration among clinicians, researchers, policymakers, and patients will be essential to realize its full potential.

Pharmacogenomics truly exemplifies the shift toward precision medicine, where treatments are designed for individuals based on their genetic profile, leading to better health outcomes for patients and a more efficient healthcare system.

Acknowledgements

Competing Interests: All the authors declare that they have no conflict of interest.

Ethics approval and consent to participate: Not applicable.

Consent for publication: Not applicable.

Availability of data and material: All the resources consulted in the review are provided in the reference section.

Funding: No funding of any kind was received.

Authors' contributions: This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Disclaimer (Artificial intelligence): Author(s) hereby declare that generative AI technologies such as large language models (ChatGPT) was used in language structure of some parts of this paper.

References

1. Cecchin E, Stocco G. Pharmacogenomics and personalized medicine. Genes. 2020;11(6):679. DOI: 10.3390/genes11060679
2. MedlinePlus. What is pharmacogenomics? [Internet]. [cited 2025 May 10]. Available from: https://medlineplus.gov/genetics/understanding/genomicresearch/pharmacogenomics/

3. Zhang G, Nebert DW. Personalized medicine: Genetic risk prediction of drug response. Pharmacol Ther. 2017;175:75–90. DOI: 10.1016/j.pharmthera.2017.02.036
4. Schwarz UI, Gulilat M, Kim RB. The role of next-generation sequencing in pharmacogenetics and pharmacogenomics. Cold Spring Harb Perspect Med. 2019;9(2):a033027. DOI: 10.1101/cshperspect.a033027
5. Caudle KE, Dunnenberger HM, Freimuth RR, Peterson JF, Burlison JD, Whirl-Carrillo M, et al. Standardizing terms for clinical pharmacogenetic test results: consensus terms from the Clinical Pharmacogenetics Implementation Consortium (CPIC). Genet Med. 2017;19(2):215–23. DOI: 10.1038/gim.2016.87
6. Johnson JA. Pharmacogenetics in clinical practice: how far have we come and where are we going? Pharmacogenomics. 2013;14(7):835–43. DOI: 10.2217/pgs.13.52
7. Saunders H, Harris D, Chirilă RM. Pharmacogenomics: introduction and use in clinical practice. Rom J Intern Med. 2020;58(2):69–74. DOI: 10.2478/rjim-2020-0001
8. Ernstmeyer K, Christman E, editors. Nursing Pharmacology [Internet]. 2nd ed. Eau Claire (WI): Chippewa Valley Technical College; 2023. Chapter 1, Pharmacokinetics & Pharmacodynamics. Available from: https://www.ncbi.nlm.nih.gov/books/NBK595006/
9. Li Y, Meng Q, Yang M, Liu D, Hou X, Tang L, et al. Current trends in drug metabolism and pharmacokinetics. Acta Pharmaceutica Sinica B. 2019;9(6):1113–44. DOI: 10.1016/j.apsb.2019.10.001
10. Aka I, Bernal CJ, Carroll R, Maxwell-Horn A, Oshikoya KA, Van Driest SL. Clinical pharmacogenetics of cytochrome P450-associated drugs in children. J Pers Med. 2017;7(4):14. DOI: 10.3390/jpm7040014
11. Orrico KB. Basic Concepts in Genetics and Pharmacogenomics for Pharmacists. Drug Target Insights. 2019;13:1177392819886875. DOI: 10.1177/1177392819886875
12. López-Fernández LA. ATP-Binding Cassette Transporters in the Clinical Implementation of Pharmacogenetics. J Pers Med. 2018;8(4):40. DOI: 10.3390/jpm8040040
13. Elbahnsi A, Dudas B, Callebaut I, Hinzpeter A, Miteva MA. ATP-Binding Cassette and Solute Carrier Transporters: Understanding Their Mechanisms and Drug Modulation Through Structural and Modeling Approaches. Pharmaceuticals. 2024;17(12):1602. DOI: 10.3390/ph17121602
14. Ataseven E, Kosova B, Aktan Ç, Kurugöl Z, Kantar M. Thiopurine-S-methyltransferase gene polymorphism and drug-related toxicity in children treated for acute leukemia and non-Hodgkin's lymphoma. J Pediatr Res. 2022;9(1):60–65. DOI: 10.4274/jpr.galenos.2021.35492
15. Abaji R, Krajinovic M. Thiopurine S-methyltransferase polymorphisms in acute lymphoblastic leukemia, inflammatory bowel disease and autoimmune disorders: influence on treatment response. Pharmacogenomics Pers Med. 2017;10:143–156. DOI: 10.2147/PGPM.S108123
16. Lee S, Jeong Y, Hong D, et al. Clinical impact of CYP2C19 genotype on clopidogrel-based antiplatelet therapy after percutaneous coronary intervention. J Am Coll Cardiol Intv. 2023;16(7):829–843. DOI: 10.1016/j.jcin.2023.01.363
17. Austin-Zimmerman I, Wronska M, Wang B, Irizar H, Thygesen JH, Bhat A, et al. The influence of CYP2D6 and CYP2C19 genetic variation on diabetes mellitus risk in people taking antidepressants and antipsychotics. Genes. 2021;12(11):1758. DOI: 10.3390/genes12111758
18. van Westrhenen R, Aitchison KJ, Ingelman-Sundberg M, Jukić MM. Pharmacogenomics of antidepressant and antipsychotic treatment: how far have we got and where are we going? Front Psychiatry. 2020;11:94. DOI: 10.3389/fpsyt.2020.00094
19. Brown SA, Pereira N. Pharmacogenomic impact of CYP2C19 variation on clopidogrel therapy in precision cardiovascular medicine. J Pers Med. 2018;8(1):8. DOI: 10.3390/jpm8010008
20. Cavallari LH, Pratt VM. Building evidence for clinical use of pharmacogenomics and reimbursement for testing. Clin Lab Med.

2022;42(4):533–546. DOI: 10.1016/j.cll.2022.09.009

21. Al-Eitan LN, Almasri AY, Khasawneh RH. Effects of CYP2C9 and VKORC1 polymorphisms on warfarin sensitivity and responsiveness during the stabilization phase of therapy. Saudi Pharm J. 2019;27(4):484–490. DOI: 10.1016/j.jsps.2019.01.011
22. Singer J, Brauneck E, Zwickl-Traxler E, Pecherstorfer M. Evaluation of personalized cancer therapies based on comprehensive genomic profiling in a middle-sized oncologic center in Austria, the University Clinic Krems. Transl Oncol. 2021;14(5):101021. DOI: 10.1016/j.tranon.2021.101021
23. Zhao J, Zhou Z, Saw PE, Song E. Silver jubilee of HER2 targeting: A clinical success in breast cancer. J Natl Cancer Center. 2025. Advance online publication. DOI: 10.1016/j.jncc.2024.12.008
24. Khani NS, Hudson G, Mills G, et al. A systematic review of pharmacogenetic testing to guide antipsychotic treatment. Nat Ment Health. 2024;2:616–626. DOI: 10.1038/s44220-024-00240-2
25. Relling M, Evans W. Pharmacogenomics in the clinic. Nature. 2015;526:343–350. DOI: 10.1038/nature15817
26. Lam JT. Infectious diseases pharmacogenomics. In: Pharmacogenomics: A Primer for Clinicians [Internet]. New York: McGraw-Hill Education; [cited 2025 May 10]. Chapter 6. Available from: https://accesspharmacy.mhmedical.com
27. Mounzer K, Hsu R, Fusco JS, Brunet L, Henegar CE, Vannappagari V, et al. HLA-B*57:01 screening and hypersensitivity reaction to abacavir between 1999 and 2016 in the OPERA® observational database: a cohort study. AIDS Res Ther. 2019;16(1):1. DOI: 10.1186/s12981-019-0217-3
28. Chan SL, Ng HY, Sung C, Chan A, Winther MD, Brunham LR, Wee HL. Economic burden of adverse drug reactions and potential for pharmacogenomic testing in Singaporean adults. Pharmacogenomics J. 2019;19(4):401–410. DOI: 10.1038/s41397-018-0053-1
29. Montemurro F, Delaloge S, Barrios CH, Wuerstlein R, Anton A, Brain E, et al. Trastuzumab emtansine (T-DM1) in patients with HER2-positive metastatic breast cancer and brain metastases: exploratory final analysis of cohort 1 from KAMILLA, a single-arm phase IIIb clinical trial. Ann Oncol. 2020;31(10):1350–8. DOI: 10.1016/j.annonc.2020.06.020
30. Yardley DA, Krop IE, LoRusso PM, Mayer M, Barnett B, Yoo B, Perez EA. Trastuzumab emtansine (T-DM1) in patients with HER2-positive metastatic breast cancer previously treated with chemotherapy and 2 or more HER2-targeted agents: results from the T-PAS expanded access study. Cancer J. 2015;21(5):357–64. DOI: 10.1097/PPO.0000000000000144
31. Qahwaji R, Ashankyty I, Sannan NS, Hazzazi MS, Basabrain AA, Mobashir M. Pharmacogenomics: A genetic approach to drug development and therapy. Pharmaceuticals. 2024;17(7):940. DOI: 10.3390/ph17070940
32. Ingelman-Sundberg M, Molden E. Therapeutic drug monitoring, liquid biopsies or pharmacogenomics for prediction of human drug metabolism and response. Br J Clin Pharmacol. 2024;1–11. DOI: 10.1111/bcp.16048
33. Dickmann LJ, Ware JA. Pharmacogenomics in the age of personalized medicine. Drug Discov Today Technol. 2016;21–22:11–6. DOI: 10.1016/j.ddtec.2016.11.003
34. Rangaraj S, Ankani BT. Warfarin Dose Maintenance Associated with CYP2C9* 2 (rs1799853) and CYP2C9* 3 (rs1057910) Gene Polymorphism in North Coastal Andhra Pradesh. Open Biochem J. 2024;18(1). DOI: 10.2174/011874091X321015240703100613
35. Chong K, Vaux KK. Warfarin Dosing and VKORC1/CYP2C9. Medscape. Updated January 12, 2021. Accessed August 2, 2025. Available from: https://emedicine.medscape.com/article/1733331-overview
36. Bellanca CM, Augello E, Cantone AF, Di Mauro R, Attaguile GA, Di Giovanni V, et al. Insight into risk factors, pharmacogenetics/genomics, and management of adverse drug reactions in elderly: a narrative review. Pharmaceuticals. 2023;16(11):1542. DOI: 10.3390/ph16111542

37. Roden DM, Wilke RA, Kroemer HK, Stein CM. Pharmacogenomics: the genetics of variable drug responses. Circulation. 2011;123(15):1661–70. DOI: 10.1161/CIRCULATIONAHA.109.914820
38. Walters S, Aldous C, Malherbe H. Knowledge, attitudes, and practices of primary healthcare practitioners in low- and middle-income countries: a scoping review on genetics. J Community Genet. 2024;15(5):461–74. DOI: 10.1007/s12687-024-00721-y
39. Institute of Medicine (US) Committee on Assessing Genetic Risks; Andrews LB, Fullarton JE, Holtzman NA, et al., editors. Assessing Genetic Risks: Implications for Health and Social Policy. Washington (DC): National Academies Press (US); 1994. Chapter 2, Genetic Testing and Assessment. Available from: https://www.ncbi.nlm.nih.gov/books/NBK236037/
40. Ausi Y, Barliana MI, Postma MJ, Suwantika AA. One step ahead in realizing pharmacogenetics in low- and middle-income countries: what should we do? J Multidiscip Healthc. 2024;17:4863–74. DOI: 10.2147/JMDH.S458564
41. Chapman CR, Mehta KS, Parent B, Caplan AL. Genetic discrimination: emerging ethical challenges in the context of advancing technology. J Law Biosci. 2019;7(1):lsz016. DOI: 10.1093/jlb/lsz016
42. Roberts JL. The Genetic Information Nondiscrimination Act as an antidiscrimination law. Notre Dame Law Rev. 2013;86(2):597–634. Available from: https://scholarship.law.nd.edu/ndlr/vol86/iss2/3
43. Haga SB, Mills R. A review of consent practices and perspectives for pharmacogenetic testing. Pharmacogenomics. 2016;17(14):1595–605. DOI: 10.2217/pgs-2016-0039
44. Khoury MJ, Bowen S, Dotson WD, Drzymalla E, Green RF, Goldstein R, et al. Health equity in the implementation of genomics and precision medicine: A public health imperative. Genet Med. 2022;24(8):1630–9. DOI: 10.1016/j.gim.2022.04.009
45. Omran S, Leong SL, Blebil A, Mohan D, Teoh SL. Effectiveness of pharmacogenomics educational interventions on healthcare professionals and health professions students: A systematic review. Res Social Adm Pharm. 2023;19(11):1399–411. DOI: 10.1016/j.sapharm.2023.07.012
46. Dwyer B. Impacts of pharmacogenomics on drug development and clinical practice. J Pharmacogenom Pharmacoproteomics. 2023;14:037. DOI: 10.35248/2153-0645.23.14.016.037
47. Rohrer Vitek CR, Abul-Husn NS, Connolly JJ, Hartzler AL, Kitchner T, Peterson JF, et al. Healthcare provider education to support integration of pharmacogenomics in practice: the eMERGE Network experience. Pharmacogenomics. 2017;18(10):1013–25. DOI: 10.2217/pgs-2017-0038
48. Hicks JK, Dunnenberger HM, Gumpper KF, Haidar CE, Hoffman JM. Integrating pharmacogenomics into electronic health records with clinical decision support. Am J Health Syst Pharm. 2016;73(23):1967–76. DOI: 10.2146/ajhp160030
49. Caudle KE, Klein TE, Hoffman JM, Muller DJ, Whirl-Carrillo M, Gong L, et al. Incorporation of pharmacogenomics into routine clinical practice: the Clinical Pharmacogenetics Implementation Consortium (CPIC) guideline development process. Curr Drug Metab. 2014;15(2):209–17. DOI: 10.2174/1389200215666140130124910
50. Cheng CM, So TW, Bubp JL. Characterization of pharmacogenetic information in Food and Drug Administration drug labeling and the Table of Pharmacogenetic Associations. Ann Pharmacother. 2021;55(10):1185–94. DOI: 10.1177/1060028020983049
51. Caudle KE, Klein TE, Hoffman JM, Muller DJ, Whirl-Carrillo M, Gong L, et al. Incorporation of pharmacogenomics into routine clinical practice: the Clinical Pharmacogenetics Implementation Consortium (CPIC) guideline development process. Curr Drug Metab. 2014;15(2):209–17. DOI: 10.2174/1389200215666140130124910
52. U.S. Pharmacist. Therapeutic application of pharmacogenomics in oncology: Selective biomarkers for cancer treatment [Internet]. U.S. Pharmacist; 2019 Aug 20 [cited 2025 May 15]. Available

from: https://www.uspharmacist.com/article/therapeutic-application-of-pharmacogenomics-in-oncology-selective-biomarkers-for-cancer-treatment

53. Delaney C, Frank S, Huang RS. Pharmacogenomics of EGFR-targeted therapies in non-small cell lung cancer: EGFR and beyond. Chin J Cancer. 2015;34(4):149–60. DOI: 10.1186/s40880-015-0007-9
54. Dunnenberger HM, Crews KR, Hoffman JM, Caudle KE, Broeckel U, Howard SC, et al. Preemptive clinical pharmacogenetics implementation: current programs in five US medical centers. Annu Rev Pharmacol Toxicol. 2015;55:89–106. DOI: 10.1146/annurev-pharmtox-010814-124835
55. Taherdoost H, Ghofrani A. AI's role in revolutionizing personalized medicine by reshaping pharmacogenomics and drug therapy. Intell Pharm. 2024;2(5):643–50. DOI: 10.1016/j.ipha.2024.08.005
56. Yuan Q, Deng D, Pan C, Ren J, Wei T, Wu Z, et al. Integration of transcriptomics, proteomics, and metabolomics data to reveal HER2-associated metabolic heterogeneity in gastric cancer with response to immunotherapy and neoadjuvant chemotherapy. Front Immunol. 2022;13:951137. DOI: 10.3389/fimmu.2022.951137
57. Burke KA, O'Sullivan J, Godfrey N, Sharma V, Hilton S, Wright SJ, et al. Development and Validation of a Rapid Point-of-Care CYP2C19 Genotyping Platform. J Mol Diagn. 2025;27(3):209–15. DOI: 10.1016/j.jmoldx.2024.12.001
58. de Olazarra AS, Wang SX. Advances in point-of-care genetic testing for personalized medicine applications. Biomicrofluidics. 2023;17(3):031501. DOI: 10.1063/5.0143311

Australian Journal of Biomedical Research
(eISSN 3083-4708)

Review Article

Hospital-Acquired Infections in the Age of Antimicrobial Resistance and Smart Surveillance

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Received: Aug 07, 2025
Accepted: Aug 13, 2025

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Abstract:
Hospital-acquired infections (HAIs) continue to be one of the biggest problems for modern healthcare systems, and the problem is getting worse because antimicrobial resistance (AMR) is on the rise. Antibiotics that used to work are quickly losing their effectiveness, which is giving rise to highly adaptable bacteria in clinical settings and turning routine procedures into high-risk situations. This publication examines the intersection of healthcare-associated infections (HAIs) and antimicrobial resistance (AMR) within the framework of smart surveillance—digital, data-driven systems engineered to identify, predict, and disrupt the spread of infections in real time. We examine the historical development of infection surveillance, analyze the epidemiological burden and resistance mechanisms contributing to a covert pandemic, and assess emerging technologies such as electronic health record integration, machine-learning analytics, genomic sequencing, and Internet of Things (IoT) sensor networks. These new ideas give us new ways to prevent infections before they happen, but they also bring up difficult moral, legal, and social problems about privacy, fairness, and governance. We contend that intelligent surveillance should be integrated into comprehensive infection prevention frameworks and antimicrobial stewardship initiatives to establish resilient hospitals. By combining predictive analytics with basic IPC procedures, ethical monitoring, and giving workers more autonomy, healthcare organizations may turn passive surveillance into active defense. In the end, winning the war against HAIs will depend not just on cutting-edge technology, but also on how it is used with care, honesty, and openness.

Keywords: Hospital-acquired infections; Antimicrobial resistance; Smart surveillance; Predictive analytics; Infection prevention and control.

Introduction

Hospitals have long been seen as safe places with precise medical care, yet they have a strange problem: diseases thrive in sterile hallways and high-tech wards without anybody noticing. These Hospital-Acquired Infections (HAIs) are infections that weren't present or incubating when the patient was admitted, but show up 48 hours or more after they have been in the hospital [1]. They happen right where healing is meant to happen. HAIs are a deadly mix of life-saving medical care and microbial opportunism. They can happen when a ventilator causes pneumonia, a catheter causes a bloodstream infection, or a surgical site is contaminated.

In the age of Antimicrobial Resistance (AMR), this issue is no longer just procedural; it is now existential. As harmful germs evolve to and evade the pharmacological arsenal that previously controlled them, therapy options diminish. Methicillin-resistant Staphylococcus aureus, carbapenem-resistant Pseudomonas and Enterobacterales, and vancomycin-resistant Enterococci have become permanent residents of ICUs, turning hospitals into places where evolution happens [2]. The clinical impact is clear: traditional treatment is becoming less and less effective against HAIs, which makes people sick longer, costs more, and kills people with ruthless efficiency.

In light of this, a new tactic has begun to take shape: smart monitoring. Surveillance systems are changing from passive storage spaces to active tools for prediction, early detection, and strategic reaction by using digital health records, quick genetic tests, sensor networks, and artificial intelligence. The knowledge collected from these interconnected platforms promises to halt transmission chains, identify high-risk circumstances before epidemics occur, and personalize interventions with unprecedented precision [3]. While this paper examines HAIs in general to provide a comprehensive view of their intersection with AMR and smart surveillance, we recognize that focusing on a single high-impact pathogen—such as methicillin-resistant Staphylococcus aureus or carbapenem-resistant Enterobacterales—could allow for an even deeper analysis. This broader scope was chosen to capture commonalities across pathogens and inform surveillance strategies applicable to multiple resistant organisms.

We hypothesize that integrating smart surveillance technologies with established infection prevention and antimicrobial stewardship strategies can significantly reduce the incidence and impact of antimicrobial-resistant HAIs in healthcare settings. The aim of this paper is to synthesize current evidence on HAIs and AMR, evaluate the role of smart surveillance technologies, and propose a conceptual framework for their integration into modern healthcare systems.

This paper contends that the convergence of antimicrobial resistance (AMR) and healthcare-associated infections (HAIs) in modern healthcare establishes a pressing necessity: only via the ethical and judicious implementation of advanced surveillance can we overcome the constraints of conventional infection control methods. By reimagining surveillance as a forward-thinking, tech-savvy part of hospital resilience, we might be able to get the upper hand on the silent killers that are in our wards. To better illustrate the complex interplay between infection risks, resistance dynamics, and technological interventions, we present a conceptual framework (Figure 1) highlighting their convergence in modern healthcare environments.

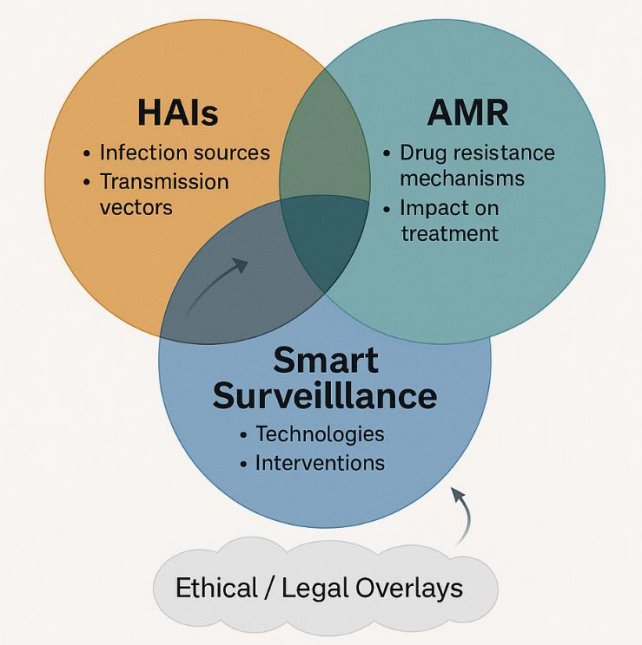

Figure 1. The Intersection of HAIs, AMR, and Smart Surveillance in Modern Healthcare. A conceptual Venn diagram illustrating the interconnected relationship between Hospital-Acquired Infections (HAIs), Antimicrobial Resistance (AMR), and Smart Surveillance. The overlapping areas highlight how these domains influence and reinforce each other. Ethical and legal considerations are depicted as an overarching layer affecting all three components.

The Epidemiological Burden of Hospital-Acquired Infections (HAIs)

The epidemiology of Hospital-Acquired Infections has changed a lot since the Crimean War, when Florence Nightingale first saw how bad hygiene could kill people. Now, hospitals have complex intensive care units full of invasive devices and patients with weakened immune systems [4]. In the 1800s, puerperal sepsis and gangrene were the most common diseases. This was mostly because people didn't practice good hygiene and didn't know how to use aseptic techniques [5].

Over time, the introduction of medicines and improvements in surgical techniques temporarily reduced these risks, but they also unintentionally created new habitats for more advanced infections. Changes in how vulnerable hosts are (older people, people with chronic illnesses, and people with weakened immune systems) and more complicated treatments (mechanical ventilation, indwelling catheters, organ transplantation) have changed the microbial battlefield, making hospitals perfect places for opportunistic infections [6].

HAIs are a big problem in today's world. The World Health Organization says that hundreds of millions of people around the world are affected each year, which means a lot of illness, extended hospital stays, and huge healthcare expenses [7]. In high-income countries, about 7–10% of hospitalized patients get at least one HAI. In low- and middle-income countries, that number might be as high as 15–20%[8]. The Centres for Disease Control and Prevention says that HAIs cause more than 1.7 million illnesses and about 100,000 deaths in the US each year, costing between $35 and $45 billion [9]. These numbers hide big differences: tertiary hospitals with strong infection control systems do far better than rural or public hospitals that don't have enough resources and are overcrowded, have poor staffing ratios, and don't have enough surveillance. Regions with few resources, especially in sub-Saharan Africa and portions of South Asia, have a harder time containing and reporting problems, and they often have to deal with more of the problems than they should [10].

A group of pathogens that are very hard to kill is in charge of the worldwide HAI landscape. Methicillin-resistant Staphylococcus aureus (MRSA) continues to produce catastrophic infections in the bloodstream and at surgical sites, while Vancomycin-resistant Enterococci (VRE) tear through oncology wards [11]. Gram-negative species, including Carbapenem-resistant Enterobacterales (CRE), Pseudomonas aeruginosa, Acinetobacter baumannii, and extended-spectrum β-lactamase (ESBL)–producing bacteria, are causing more and more illnesses that can't be treated [2]. Clostridioides difficile, which grows when antibiotics kill off gut flora, is a major cause of nosocomial diarrhea, which can be quite dangerous for older people [12].

Table 1: Prevalence of Hospital-Acquired Infections in Selected Regions and Settings

Region / Country	Study Design / Source	Reported Prevalence	Reference
High-income countries (overall)	WHO global review	7–10% of hospitalized patients	WHO, 2025 [7]
Low- and middle-income countries (overall)	WHO global review	15–20% of hospitalized patients	WHO, 2025 [7]
Nigeria	Cross-sectional, tertiary hospital	16.9% point prevalence	Abubakar et al., 2022 [8]
Bangladesh	WHO IPCAF assessment in tertiary care	11.6% average prevalence	Harun et al., 2022 [10]
United States	CDC National HAI estimates	~4.5% prevalence; 1.7 million cases annually	CDC, 2022 [9]
Central China	Multicenter case-control	5.8% prevalence	Li et al., 2022 [9]

Urinary tract infections are the most common type of infection, especially when indwelling catheters are utilized. Bloodstream infections associated to intravenous lines are the second most common type. Ventilator-associated pneumonias persist in ICUs, and

surgical site infections continue to compromise surgical outcomes despite preventive measures [13]. These infections have a big effect on people's health, finances, and emotions. They endanger not only individual patients but also the integrity of healthcare systems globally, highlighting the pressing necessity for advanced measures in prevention, detection, and control. Table 1 summarizes reported prevalence rates of HAIs in selected regions and healthcare settings, illustrating substantial variation between high-income and low- and middle-income countries.

Antimicrobial Resistance: Fueling a Silent Pandemic in Hospitals

Antimicrobial resistance (AMR) has emerged as one of the most urgent public health challenges of the 21st century, undermining decades of medical progress. The 2022 Lancet analysis on the global burden of bacterial AMR estimated 4.95 million deaths associated with drug-resistant infections in 2019 alone, with 1.27 million directly attributable to AMR [14]. WHO surveillance data further indicate that resistance rates among priority pathogens such as Klebsiella pneumoniae, Escherichia coli, Acinetobacter baumannii, and Staphylococcus aureus are increasing in nearly all regions, with the highest burden in low- and middle-income countries [15].

At the molecular level, pathogens employ several well-characterized mechanisms to evade antimicrobial activity. These include enzymatic inactivation (e.g., β-lactamases, carbapenemases), alteration of drug targets (such as penicillin-binding protein mutations in MRSA), reduced membrane permeability, increased active efflux of antimicrobial agents, and biofilm formation that shields bacteria from both drugs and host immune responses [16]. Resistance traits can be intrinsic or acquired through genetic mutation or, more importantly in healthcare settings, horizontal gene transfer [17]. Horizontal gene transfer — mediated by plasmids, integrons, and transposons — accelerates the spread of resistance determinants within and across bacterial species. Mobile genetic elements frequently carry multiple resistance genes, enabling the rapid emergence of multidrug- and even pan-drug-resistant strains. Genomic investigations of hospital outbreaks have repeatedly traced their origins to plasmid-borne carbapenemase genes or vancomycin resistance operons, highlighting the urgent need for routine molecular surveillance [18], [19].

In hospitals, several factors fuel the persistence and spread of AMR. These include high selection pressure from broad-spectrum antibiotic use (often empirical), frequent use of invasive devices that provide surfaces for biofilm growth, lapses in infection prevention and control during periods of patient surges, and delays in laboratory detection that allow resistant organisms to circulate undetected. The COVID-19 pandemic amplified many of these drivers, with increased antibiotic prescribing and resource diversion contributing to spikes in certain multidrug-resistant hospital-onset infections.

The clinical consequences are profound: AMR-associated HAIs are linked to higher mortality, prolonged hospital stays, more frequent readmissions, and significantly higher treatment costs. In resource-limited settings, the lack of rapid diagnostics and limited antimicrobial options further exacerbates these impacts.

Given this escalating threat, traditional passive surveillance and delayed laboratory reporting are insufficient. Proactive, technology-enhanced approaches — including real-time genomic sequencing, automated data analytics, and AI-assisted prediction — are increasingly essential to detect, characterize, and respond to resistant pathogens before outbreaks escalate [20], [21].

Specific case examples show how serious the situation is. Extended-spectrum β-lactamase (ESBL) generating Enterobacterales like Escherichia coli and Klebsiella pneumoniae are increasingly common in many tertiary hospitals across the world. They make whole classes of cephalosporins and penicillins useless. In response, carbapenems—once considered as last-resort agents—have seen growing use, which has, in turn, given rise to carbapenemase-producing organisms (CPOs) such as KPC- and NDM-producing Klebsiella and Enterobacter spp., now recognized as some of the most serious nosocomial dangers [22]. Even more worrying is the rise of pan-resistant strains, which are bacteria that are resistant to all existing antimicrobials. This has already been seen with Acinetobacter baumannii and some CRE isolates. These germs can quickly change normal ICU hospitalizations into deadly situations, forcing doctors to look for

compassionate-use medications and experimental treatments [23].

These factors create a hidden epidemic that is growing behind hospital curtains. Antimicrobial resistance not only makes it harder to treat HAIs, but it also threatens the fundamental foundation of contemporary medicine. The safety of surgery, chemotherapy, transplantation, and intensive care is seriously compromised without adequate antibiotics. If strong steps aren't taken to stop the development of resistance, enforce stewardship, and use new drugs along with sophisticated surveillance, hospitals may not be able to fight illnesses that they used to readily control. This would be a step backward with terrible effects around the world [20].

Smart Surveillance Technologies: The New Frontier

Surveillance has always been an important part of preventing infections, but the mechanisms that have been used in the past—manual reporting, retrospective chart audits, and irregular laboratory notifications—have not kept up with how quickly and complicated pathogens spread in today's healthcare settings. Traditional surveillance works reactively, counting illnesses after they happen, sending out data on a regular basis, and relying a lot on people being alert. Smart surveillance, on the other hand, is a huge change towards proactive, data-driven defense. Hospitals are changing from passive recorders of outbreaks to predictive guardians who can stop transmission before it gets out of hand by employing technology to collect, assess, and act on real-time information [24].

The technological infrastructure underpinning this revolution is multifaceted. *Electronic Health Records (EHRs)* serve as the foundational layer, aggregating clinical variables such as vital signs, imaging, laboratory diagnostics, antimicrobial prescriptions, and procedural data. When harnessed through automated surveillance platforms, these datasets can be continuously mined for anomalies suggestive of early infection—eliminating delays inherent in manual review processes. In essence, every patient interaction becomes a point of surveillance, quietly feeding into a hospital-wide nervous system attuned to infection risk [25]. To visualize how data flows through a smart surveillance network, Figure 2 maps the interconnected components of a hospital's digital infrastructure and their roles in infection prevention.

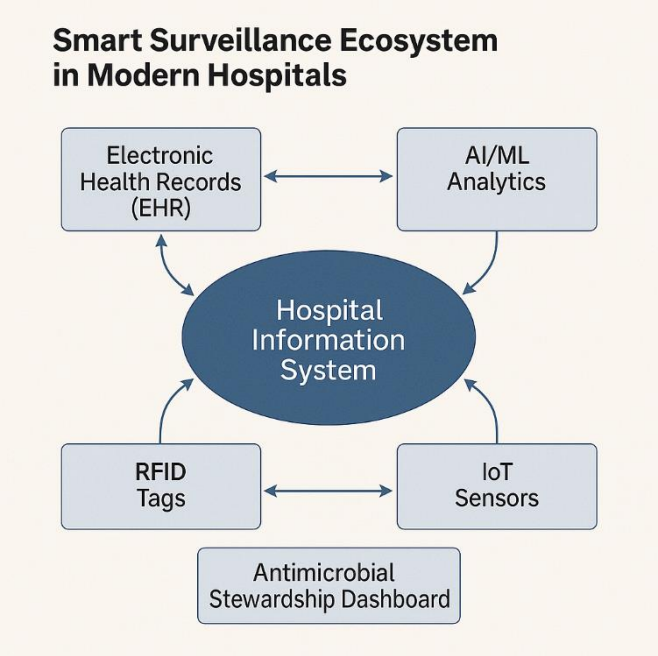

Figure 2. Smart Surveillance Ecosystem in Modern Hospitals. This systems diagram illustrates the core components of a smart surveillance infrastructure in hospitals. The central Hospital Information System serves as the nexus, integrating data from Electronic Health Records (EHR), Artificial Intelligence and Machine Learning (AI/ML) analytics, Whole Genome Sequencing (WGS) labs, Internet of Things (IoT) sensors, RFID tracking systems, and the Antimicrobial Stewardship Dashboard to enable real-time infection detection and intervention.

The interpretive power of this data lies increasingly in *Artificial Intelligence (AI)* and *Machine Learning (ML)*. These tools ingest massive, multidimensional datasets to identify complex patterns and correlations. Instead of flagging infections only after microbiological confirmation, AI algorithms can predict outbreak trajectories based on subtle shifts—an uptick in specific antibiotic orders, a cluster of fevers in a particular ward, or deviations from expected recovery trajectories. Such predictive insights allow infection-control teams to deploy interventions (e.g., enhanced

cleaning, cohorting, isolation, or prophylaxis adjustments) in a preemptive, targeted fashion [26].

At the same time, genetic technologies are changing how well we can find things. Whole-Genome Sequencing (WGS) gives a clear picture of microbial "fingerprinting," which lets hospital epidemiologists figure out if two diseases came from the same strain or from different sources. This helps quickly find transmission networks and tell the difference between real outbreaks and random occurrences. Metagenomic sequencing can read all of the genetic material in a sample. It can find organisms that are not expected or cannot be cultured, and it can also find resistance genes before they show up in the phenotype. As sequencing platforms get quicker and cheaper, it's easier to use them for real-time surveillance [27].

Sensor-based technologies from the Internet of Things (IoT) are adding to these analytical capabilities. Smart hand hygiene systems have sensors that talk to staff ID cards and keep track of how well units are washing their hands [28]. If a unit doesn't wash their hands properly, the system sends rapid feedback. Environmental sensors keep an eye on microbial contamination on surfaces that people touch a lot and in ventilation systems. They let cleaning workers know when they need to act before infections can build up in strongholds. Radio-Frequency Identification (RFID) tags on equipment, staff badges, and patients monitor the movement and contact networks across the hospital environment [29]. This makes it easy to quickly trace exposure pathways if there is a suspected case of cross-transmission. Together, these devices act like millions of eyes and ears, always watching the micro-environment with a level of accuracy that no human worker could match. To facilitate rapid comparison, Table 2 summarizes the key smart surveillance tools discussed above, their primary functions, and documented impacts in healthcare settings.

Table 2. Key Smart Surveillance Tools, Functions, and Documented Impacts

Tool	Primary Function	Documented Impact
Electronic Health Records (EHRs)	Aggregate patient data (vitals, labs, imaging, prescriptions) for automated anomaly detection	Reduced detection delays; improved outbreak response speed in NHSN-participating hospitals
Artificial Intelligence / Machine Learning (AI/ML)	Predict infection trends from multidimensional datasets	Enabled targeted, preemptive interventions; reduced central-line bloodstream infections in U.S. hospitals
Whole-Genome Sequencing (WGS)	Identify microbial strains and resistance genes in real time	Accelerated outbreak source tracing; reduced MRSA and CPE clusters in NHS England
Internet of Things (IoT) Sensors	Monitor hand hygiene, environmental contamination, air quality	Improved compliance rates; reduced contamination of high-touch surfaces
Radio-Frequency Identification (RFID)	Track movement of staff, patients, and equipment	Enabled rapid contact tracing; halted carbapenem-resistant pathogen outbreaks in Singapore

Smart surveillance technologies are starting to show real results in healthcare systems all over the world. NHS England has set up digital monitoring platforms with WGS capacity, which help hospitals find and stop MRSA and CPE (carbapenemase-producing Enterobacterales) clusters faster and more effectively than ever before[30]. More and more hospitals in the United States that are part of the CDC's National Healthcare Safety Network (NHSN) are using automated data feeds and predictive analytics [31]. This has led to fewer catheter-associated urinary tract infections and central-line bloodstream infections. Singapore's health system was the first to use RFID and digital contact tracing throughout the whole institution to stop the spread of carbapenem-resistant pathogens [32]. This method is credited with stopping multiple outbreaks before they could get worse. At the same time, Scandinavian countries have used national health registries and machine-learning decision assistance to

get some of the lowest rates of multidrug-resistant HAIs in the world.

Recent evaluations have quantified the impact of AI-driven surveillance on infection prevention. For example, a multicenter U.S. study using machine learning algorithms integrated with electronic health records demonstrated a 32% reduction in central line-associated bloodstream infections and a 22% reduction in catheter-associated urinary tract infections over 18 months compared to baseline rates [33]. Similarly, in a pilot program in two Singapore tertiary hospitals, AI-based predictive models accurately identified 87% of impending multidrug-resistant organism outbreaks up to 72 hours before conventional methods [34]. These findings underscore that, beyond theoretical promise, AI-enhanced surveillance can deliver measurable clinical benefits when combined with robust infection prevention practices.

These technologies together herald the beginning of a new era of surveillance, where data flows constantly, signals are analyzed by algorithms, and reactions are quick, accurate, and based on data. As antimicrobial resistance continues to weaken the effectiveness of our treatments, the ability to detect and stop the spread of pathogens before they happen may become the most important thing that keeps hospitals safe. Smart surveillance isn't just an upgrade to our tools; it's a whole new way of thinking about how we keep an eye on, predict, and eventually control the risks we can't see in our wards [35].

Infection Prevention & Control in the Smart Era

Traditional infection prevention and control (IPC) techniques are being redesigned in today's digitally altered hospital context to capitalize on the power of smart surveillance data [36]. Foundational procedures such as thorough hand hygiene, patient isolation, bundle care techniques, and rigorous environmental cleaning remain the cornerstones of IPC, but they are increasingly being optimized via real-time feedback loops [37]. Hand hygiene, which was formerly monitored irregularly by ward observers, can now be recorded continually using sensor-equipped dispensers and badge-linked compliance systems. Isolation techniques are constantly deployed based on predictive data that detect high-risk individuals early, often before clinical symptoms appear [38]. Care bundles for central line care, ventilator use, and urine catheters are audited against live dashboards rather than quarterly reports, allowing teams to intervene quickly when adherence falters. Environmental cleaning has also evolved: pollution reports guide ultraviolet disinfection robots, ATP bioluminescence swabs, and surface-mapping tools, directing resources towards growing hotspots rather than following static timetables [39].

When these established interventions are combined with adaptive protocols informed by surveillance data, their value increases significantly. Rather than relying on blanket treatments, hospitals are increasingly utilizing tailored decolonization tactics, such as screening at-risk patients with quick diagnostics and strategically delivering nasal mupirocin or chlorhexidine washes where they are most effective [40]. Situational alerts created by digital surveillance platforms warn doctors when patients colonized or infected with resistant pathogens are admitted or transferred, immediately initiating isolation orders and tailored precautions. For example, when microbiology systems discover and electronically flag a patient with carbapenem-resistant Klebsiella pneumoniae, automated alerts are sent to bed managers, environmental services and chemists, tightening the net around potential transmission points [41].

Antimicrobial Stewardship Programs (ASPs) play an increasingly important role in the smart IPC environment. Integrating prescribing analytics with resistance surveillance outputs allows stewardship teams to update formulary guidance in real time, encouraging doctors towards narrow-spectrum medicines or alternate regimens as resistance tendencies spike [42]. Smart systems enable the early detection of unsuitable empirical combinations, excessive durations, and duplicated coverage, resulting in "stepped-down" therapy. What was to be a lengthy chart review is now guided by computerized dashboards that span inpatient wards, outpatient clinics, emergency departments, and surgical suites, allowing for more rational antibiotic usage across the whole care continuum. In doing so, ASPs not only slow the development of resistance but also reduce ecological disruption, reducing the risk of opportunistic infections like Clostridium difficile [43].

Maintaining such improvements necessitates a continued emphasis on education and behavioral change among healthcare staff. Smart surveillance data

is most effective when it is converted into actionable intelligence for front-line personnel. Real-time feedback panels in staff areas display unit-specific infection trends and compliance performance, promoting transparency and responsibility. Simulation training modules based on recent outbreak scenarios promote a proactive mindset, while targeted reminders and behavior-nudging cues help maintain adherence. Professional development programs now include data interpretation training, resulting in a new breed of infection-control-literate clinicians capable of collaborating with digital systems rather than merely being monitored by them [44].

Finally, infection prevention in the smart era moves beyond compliance with static protocols and into an adaptive, learning system in which clinical teams respond dynamically to changing microbial threats. By combining known IPC methods with continuous surveillance, real-time decision support, antimicrobial stewardship, and empowered healthcare personnel, hospitals may go from reacting to infections to preventing them with accuracy. This symbiotic interaction between human vigilance and technology intelligence is at the heart of robust, future-ready healthcare systems that can tackle the ever-changing threats of antimicrobial-resistant HAIs [45].

Ethical, Legal, and Socio-cultural Challenges

As hospitals embrace smart surveillance as a crucial weapon against antimicrobial-resistant illnesses, they must also deal with a complicated set of ethical, legal, and socio-cultural issues. The most pressing of these concerns is privacy and autonomy. Smart surveillance systems rely on the constant aggregation of sensitive patient data (diagnoses, microbiological results, medication histories, and genomic data), generating valid concerns about data security, consent, and potential abuse [20]. Ensuring strong encryption, access restrictions, and governance frameworks is critical to preventing breaches or patient re-identification. At the same time, several systems monitor healthcare personnel directly, recording hand hygiene, patient encounters, and location changes using RFID badges [46]. While essential for infection prevention, such monitoring blurs the distinction between professional accountability and intrusive oversight, raising concerns about autonomy and workplace surveillance [47].

These challenges are exacerbated by algorithmic biases in data interpretation. AI-powered systems are only as effective as the data on which they are trained. Biases caused by skewed data, such as under-representation of minority populations or atypical clinical presentations, might result in false positives, unneeded isolation, or unintentional neglect of persons who do not fit algorithmic standards [48]. Furthermore, hospitals in resource-rich contexts generate significantly more robust datasets than those in low-resource areas, potentially resulting in monitoring technologies that are inapplicable or inaccurate when exported. Institutions that do not provide high-quality data may be marked for risk or excluded from technology breakthroughs, exacerbating already existent discrepancies in infection control outcomes [49].

Indeed, worldwide imbalance in access to smart surveillance technologies threatens to exacerbate the digital divide in infection prevention. Wealthy healthcare systems in the Global North are progressively implementing WGS, real-time dashboards, and IoT networks, whereas hospitals in the Global South frequently lack dependable internet connectivity, standardized electronic records, or staff qualified to comprehend complex data outputs. This discrepancy risks resulting in a sort of "digital colonialism," in which surveillance techniques are created, piloted, and perfected in wealthy settings before being exported—without adequate adaptation—to countries with significantly different infrastructural or epidemiological conditions [50]. As seen in Figure 3, worldwide inequalities in digital infrastructure and technological capacity result in uneven preparation for smart surveillance systems.

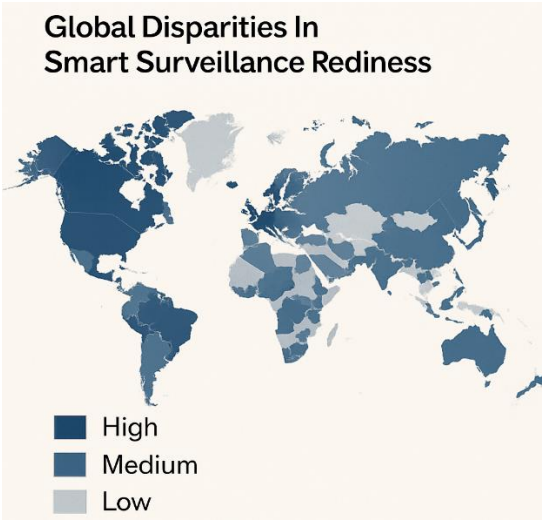

Figure 3. Global Disparities in Smart Surveillance Readiness. A choropleth world map showing country-level differences in readiness for adopting smart surveillance technologies. Nations are categorized as having high, medium, or low readiness based on infrastructure, data systems, and digital health capabilities. This map illustrates the stark digital divide that may hinder equitable infection control and antimicrobial resistance mitigation.

Finally, the success of any monitoring initiative is dependent on public confidence and transparency. Patients and staff must understand why they are being monitored, how that information is used, and what measures are in place to protect their interests. Clear, proactive communication of surveillance goals—preventing outbreaks, protecting vulnerable patients, and enhancing care—helps build buy-in while alleviating concerns about punitive or discriminating practices. Without such transparency, even technologically better systems may fail owing to opposition, fear, or disengagement from individuals they are supposed to protect [51].

Achieving the full potential of smart monitoring necessitates not only technological expertise, but also rigorous ethical stewardship—balancing infection prevention with respect for rights, equity, and trust within the medical community.

Challenges Policy and Governance Frameworks

The quick rise of smart surveillance technologies in infection control has led to big changes in policy and governance at the international, national, and institutional levels. Global groups have been very important in establishing conventions and making standards more consistent. The World Health Organization's Global Action Plan on Antimicrobial Resistance stresses the need for integrated surveillance systems and data exchange as key parts of controlling infections. It also encourages member states to use digital tools to improve early detection [52]. The U.S. Centres for Disease Control and Prevention (CDC) has also given detailed instructions for electronic reporting through its National Healthcare Safety Network (NHSN)[53]. The European Union, on the other hand, enforces surveillance reporting requirements through directives like EARS-Net and HAITool, which help make sure that systems work together across borders and set standards [54].

Government-backed stewardship and surveillance programs are very important for effective infection control at the national level. A lot of countries now mandate hospitals to report certain HAIs and resistant infections. This is linked to accreditation or reimbursement programs. The U.S. Hospital-Acquired Condition Reduction Program and the U.K.'s Commissioning for Quality and Innovation (CQUIN) are examples of funding incentives that encourage hospitals to spend money on better data infrastructure and hire more people to watch over it [55]. There are now certification systems for "digital-ready" or "infection-resilient" hospitals. These programs identify hospitals that successfully combine surveillance with IPC and antimicrobial stewardship. Public-private collaborations are becoming more and more important for innovation and growth [56].

Hospitals, technology suppliers, and pharmaceutical companies working together make it possible to quickly make prototypes of IoT devices, predictive software, and genomic sequencing platforms that are perfect for clinical operations. Industry involvement gives the money and technical know-how needed to establish interoperability standards, cybersecurity tools, and next-generation diagnostics. Healthcare systems, on the other hand, give companies places to test their products and data to improve them. But these alliances need strong governance to protect data ownership, work out intellectual property rights, and make sure that business interests don't get in the way of public health priorities [57].

Overall, achieving effective governance in the smart surveillance era requires a delicate balancing act—aligning technological progress with regulatory oversight, fostering innovation through collaboration, and ensuring that policies remain responsive to evolving epidemiological and ethical realities worldwide.

Future Horizons: Toward Smart, Resilient Hospitals

As hospitals deal with the increasing complexity of illnesses that are resistant to antibiotics, the direction of innovation is towards institutions that are not only reactive but also naturally strong. Central to this trend is the growth of AI-driven decision support systems capable of powering tailored infection control

[58]. Future platforms will go beyond interventions that affect whole populations to provide precision prevention. They will do this by dynamically assessing each patient's risk profile and adjusting prophylaxis, isolation intensity, and environmental controls as needed. Instead of treating all patients in a hospital the same way, algorithms will sort them based on their genomic vulnerability, physiological status, and exposure history. This will make the best use of resources while providing the most protection [20].

The creation of interoperable data ecosystems that go beyond just one institution is very important for this intelligence. When signs of an outbreak appear, interconnected hospital networks and regional health systems can work together to act as early warning systems. Real-time tracking of pathogen transmission between facilities, from long-term care to tertiary centres, will allow for coordinated measures instead of isolated responses. Cloud-based monitoring, shareable antibiograms, and real-time reporting pipelines will be the main tools for keeping everyone in the region up to date on what's going on [59].

But resilience isn't just about technology; it's also about the environment. As climate change changes how infectious diseases spread, hospitals need to use long-lasting new ideas in their infection management. Changes in temperature and humidity can make pathogens last longer on surfaces, and extreme weather can break supply systems and fill up emergency rooms. It is important to make sure that green hospital programs that make the hospital more energy-efficient, cut down on waste, and make the best use of resources do not put microbiological safety at risk. Advanced HVAC systems, UV sterilization built into air, and eco-friendly disinfectants can help the environment and lower the risk of infection at the same time [60].

Lastly, hospitals of the future will be physically redesigned to be more resistant to infections. Architectural design will put natural light, negative-pressure isolation suites, and modular ward layouts that can easily expand or separate during outbreaks at the top of the list. From the blueprints to the building, airflow engineering, antimicrobial surface materials, and patient flow logistics will be built in. This will turn walls, hallways, and clinical spaces into silent collaborators in infection control. All of these possibilities are coming together to create a new form of hospital: an intelligent, adaptable ecosystem that detects, predicts, and protects against microbial dangers while also protecting the human, environmental, and operational aspects of healthcare delivery [61]. In these kinds of places, infection control will be less of a job and more of a built-in part of the system.

Conclusion

In the past, hospital-acquired infections were manageable problems, but now they are serious dangers because of antibiotic resistance and microbes adapting in ways that have never happened before [62]. These quiet assassins do well in the very places that are supposed to protect life, taking advantage of complicated procedures, weak points in treatment, and blind spots in surveillance. Basic infection control measures are still very important, but the current situation is so urgent that we need to move beyond traditional methods. Smart surveillance technologies, which use real-time analytics, genetic intelligence, AI prediction, and sensor-enabled settings, give us a whole new set of tools. But their promise can only be kept if they are used together with careful infection control measures and smart antimicrobial management. Not only should the hospital of the future treat infections, it should also be able to see them coming, stop them, and outsmart them [63]. This requires not only investment in technology but also moral vigilance, strong leadership in policy, giving workers more authority, and fairness around the world. The message is clear: healthcare systems need to make smart monitoring a major part of their strategy and put it next to IPC and stewardship to make hospitals that are naturally robust, adaptable, and always learning. Technology alone won't win the war against diseases that people get in hospitals. Instead, it will be a combination of new ideas, constant watchfulness, and responsible leadership. To safeguard, heal, and defend the sanctity of life, we must make sure that every monitor, algorithm, and intervention supports the deeper purpose of medicine

Acknowledgements

AI Assistance Disclosure: Portions of this manuscript's drafting and language refinement were assisted by an

artificial intelligence language model. All content was reviewed, verified, and edited by the authors to ensure accuracy and adherence to the journal's guidelines.

Author Contributions: Olabisi Promise Lawal: Conceptualization, literature search, manuscript drafting, critical revisions, overall supervision. Idris Olumide Orenolu: Writing – review & editing, infection control expertise, literature synthesis. Morayo Anne Ajobiewe: Literature search, drafting (nursing and IPC perspectives), review & editing. Kwesi Akonu Adom Mensah Forson: Writing – review & editing, epidemiological analysis, data interpretation. Ujunwa Favour Agu: Literature contribution (nursing sciences), review & editing. Moses Emmanuel Fidelix: Data curation, drafting (laboratory diagnostics), review & editing. Frances Chinaechekwa Madugba: Contribution to microbiology sections, manuscript review. Lenin Ifeanyi Obi: Drafting (nursing and clinical application), review & editing. All authors read and approved the final manuscript.

Disclosures: The authors declare no conflicts of interest.

Acknowledgments: The authors acknowledge the contributions of all healthcare professionals and institutions whose work and data informed this review. Special thanks to colleagues who provided insights into infection prevention and control practices across diverse healthcare settings.

Funding: This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Ethics Approval: Not applicable. This study is a narrative review and did not involve human participants, animal subjects, or identifiable personal data.

References

1. Okonkwo PI, Okafor KC, Garbal JH, Kwaghal BS, Boluwatito B. Hospital Acquired Infections (HAIs) Prevention Practices Among Medical Students in a Teaching Hospital in Jos, Plateau State, Nigeria. Eur J Med Health Sci. 2024;6(2):14-20. DOI: 10.24018/ejmed.2024.6.2.1917
2. Salam MdA, Al-Amin MdY, Salam MT, Pawar JS, Akhter N, Rabaan AA, et al. Antimicrobial Resistance: A Growing Serious Threat for Global Public Health. Healthcare (Basel). 2023;11(13):1946. DOI: 10.3390/healthcare11131946
3. Yeung AWK, Torkamani A, Butte AJ, Glicksberg BS, Schuller B, Rodriguez B, et al. The promise of digital healthcare technologies. Front Public Health. 2023;11:1196596. DOI: 10.3389/fpubh.2023.1196596
4. Kolagari S. Increasing Importance of Florence Nightingale's Theory During the 21st-Century Pandemic Period. Florence Nightingale J Nurs. 2023;31(3):215-6. DOI: 10.5152/FNJN.2023.23040
5. Poczai P, Karvalics LZ. The little-known history of cleanliness and the forgotten pioneers of handwashing. Front Public Health. 2022;10:979464. DOI: 10.3389/fpubh.2022.979464
6. Quiros-Roldan E, Sottini A, Natali PG, Imberti L. The Impact of Immune System Aging on Infectious Diseases. Microorganisms. 2024;12(4):775. DOI : 10.3390/microorganisms12040775
7. World Health Organization. The burden of health care-associated infection worldwide. [Internet]. 2025 [cited 2025 Aug 5]. Available from: https://www.who.int/news-room/feature-stories/detail/the-burden-of-health-care-associated-infection-worldwide
8. Abubakar U, Amir O, Rodríguez-Baño J. Healthcare-associated infections in Africa: a systematic review and meta-analysis of point prevalence studies. J Pharm Policy Pract. 2022;15(1):99. DOI: 10.1186/s40545-022-00498-w
9. Li P, Li Y, Zhang Y, Bao J, Yuan R, Lan H, et al. Economic burden attributable to healthcare-associated infections in tertiary public hospitals of Central China: a multi-centre case-control study. Epidemiol Infect. 2022;150:e155. DOI: 10.1017/S0950268822001310

10. Harun MdGD, Anwar MMU, Sumon SA, Hassan MZ, Haque T, Mah-E-Muneer S, et al. Infection prevention and control in tertiary care hospitals of Bangladesh: results from WHO infection prevention and control assessment framework (IPCAF). Antimicrob Resist Infect Control. 2022;11:125. DOI: 10.1186/s13756-022-01165-0
11. Calfee DP. Methicillin-resistant Staphylococcus aureus and vancomycin-resistant enterococci, and other Gram-positives in healthcare. Curr Opin Infect Dis. 2012;25(4):385-94. DOI: 10.1097/QCO.0b013e3283553441
12. Jump RL. Clostridium difficile infection in older adults. Aging Health. 2013;9(4):403-14. DOI: 10.2217/ahe.13.37
13. Bouhrour N, Nibbering PH, Bendali F. Medical Device-Associated Biofilm Infections and Multidrug-Resistant Pathogens. Pathogens. 2024;13(5):393. DOI: 10.3390/pathogens13050393
14. Murray S, Gale F, Adams D, Dalton L. A scoping review of the conceptualisations of food justice. Public Health Nutr. 2023;26(4):725-37. DOI: 10.1017/S1368980022002620
15. Seid M, Bayou B, Aklilu A, Tadesse D, Manilal A, Zakir A, et al. Antimicrobial resistance patterns of WHO priority pathogens at general hospital in Southern Ethiopia during the COVID-19 pandemic, with particular reference to ESKAPE-group isolates of surgical site infections. BMC Microbiol. 2025;25:84. DOI: 10.1186/s12866-025-03054-9
16. Tao S, Chen H, Li N, Wang T, Liang W. The Spread of Antibiotic Resistance Genes In Vivo Model. Can J Infect Dis Med Microbiol. 2022;2022:3348695. DOI: 10.1155/2022/3348695
17. Yamin D, Uskoković V, Wakil AM, Goni MD, Shamsuddin SH, Mustafa FH, et al. Current and Future Technologies for the Detection of Antibiotic-Resistant Bacteria. Diagnostics (Basel). 2023;13(20):3246. DOI: 10.3390/diagnostics13203246
18. Galgano M, Pellegrini F, Catalano E, Capozzi L, Del Sambro L, Sposato A, et al. Acquired Bacterial Resistance to Antibiotics and Resistance Genes: From Past to Future. Antibiotics. 2025;14(3):222. DOI: 10.3390/antibiotics14030222
19. Skender K, Machowska A, Khare S, Singh V, Lundborg CS, Sharma M. Antibiotic prescribing practices, perceived constraints, and views on antimicrobial resistance among general and orthopedic surgeons in central India. Sci Rep. 2025;15:25099. DOI: 10.1038/s41598-025-74525-8
20. Muteeb G, Rehman MT, Shahwan M, Aatif M. Origin of Antibiotics and Antibiotic Resistance, and Their Impacts on Drug Development: A Narrative Review. Pharmaceuticals. 2023;16(11):1615. DOI: 10.3390/ph16111615
21. Kumar NR, Balraj TA, Kempegowda SN, Prashant A. Multidrug-Resistant Sepsis: A Critical Healthcare Challenge. Antibiotics (Basel). 2024;13(1):46. DOI: 10.3390/antibiotics13010046
22. Husna A, Rahman MdM, Badruzzaman ATM, Sikder MH, Islam MR, Rahman MdT, et al. Extended-Spectrum β-Lactamases (ESBL): Challenges and Opportunities. Biomedicines. 2023;11(11):2937. DOI: 10.3390/biomedicines11112937
23. Lodise TP, Nguyen ST, Margiotta C, Cai B. Clinical burden of Acinetobacter baumannii, including carbapenem-resistant A. baumannii, in hospitalized adult patients in the USA between 2018 and 2022. BMC Infect Dis. 2025;25(1):549. DOI: 10.1186/s12879-025-12345-2
24. Shenoy ES, Branch-Elliman W. Automating surveillance for healthcare-associated infections: Rationale and current realities (Part I/III). Antimicrob Steward Healthc Epidemiol. 2023;3(1):e25. DOI: 10.1017/ash.2023.156
25. Negro-Calduch E, Azzopardi-Muscat N, Krishnamurthy RS, Novillo-Ortiz D. Technological progress in electronic health record system optimization: Systematic review of systematic literature reviews. Int J Med Inform. 2021;152:104507. DOI: 10.1016/j.ijmedinf.2021.104507
26. Hudu SA, Alshrari AS, Abu-Shoura EJI, Osman A, Jimoh AO. A Critical Review of the Prospect

of Integrating Artificial Intelligence in Infectious Disease Diagnosis and Prognosis. Interdiscip Perspect Infect Dis. 2025;2025:6816002. DOI: 10.1155/2025/6816002

27. Vashisht V, Vashisht A, Mondal AK, Farmaha J, Alptekin A, Singh H, et al. Genomics for Emerging Pathogen Identification and Monitoring: Prospects and Obstacles. BioMedInformatics. 2023;3(4):1145-77. DOI: 10.3390/biomedinformatics3040069
28. Wu J, Lin Y, Lee S, Chen C, Cheng S, Cheng C, et al. IoT-Based Hand Hygiene Compliance Monitoring System and Validation of Its Effectiveness in Hospital Environments. Glob Chall. 2024;8(12):2400124. DOI: 10.1002/gch2.202400124
29. Profetto L, Gherardelli M, Iadanza E. Radio Frequency Identification (RFID) in health care: where are we? A scoping review. Health Technol (Berl). 2022;12(5):879-91. DOI: 10.1007/s12553-022-00683-6
30. Fox JM, Saunders NJ, Jerwood SH. Economic and health impact modelling of a whole genome sequencing-led intervention strategy for bacterial healthcare-associated infections for England and for the USA. Microb Genom. 2023;9(8):mgen001087. DOI: 10.1099/mgen.0.001087
31. Shenoy ES, Branch-Elliman W. Automating surveillance for healthcare-associated infections: Rationale and current realities (Part I/III). Antimicrob Steward Healthc Epidemiol. 2023;3(1):e25. DOI: 10.1017/ash.2023.156
32. Obama BM, Grant R, Harbarth S, Buetti N, Catho G. Digitalised measures for the prevention of central line-associated bloodstream infections: a scoping review. Antimicrob Resist Infect Control. 2025;14:45. DOI: 10.1186/s13756-025-00945-4
33. Shenoy S, Jena A, Levinson C, Sharma V, Deepak P, Aswani-Omprakash T, et al. Inflammatory bowel disease in south Asia: a scoping review. Lancet Gastroenterol Hepatol. 2025;10(3):259-74. DOI: 10.1016/S2468-1253(24)00356-8
34. Danchin A. Artificial intelligence-based prediction of pathogen emergence and evolution in the world of synthetic biology. Microb Biotechnol. 2024;17(10):e70014. DOI: 10.1111/1751-7915.14399
35. Yamin D, Uskoković V, Wakil AM, Goni MD, Shamsuddin SH, Mustafa FH, et al. Current and Future Technologies for the Detection of Antibiotic-Resistant Bacteria. Diagnostics (Basel). 2023;13(20):3246. DOI: 10.3390/diagnostics13203246
36. Arzilli G, De Vita E, Pasquale M, Carloni LM, Pellegrini M, Di Giacomo M, et al. Innovative Techniques for Infection Control and Surveillance in Hospital Settings and Long-Term Care Facilities: A Scoping Review. Antibiotics. 2024;13(1):77. DOI: 10.3390/antibiotics13010077
37. Alhumaid S, Al Mutair A, Al Alawi Z, Alsuliman M, Ahmed GY, Rabaan AA, et al. Knowledge of infection prevention and control among healthcare workers and factors influencing compliance: a systematic review. Antimicrob Resist Infect Control. 2021;10:86. DOI: 10.1186/s13756-021-00957-0
38. Wang C, Jiang W, Yang K, Yu D, Newn J, Sarsenbayeva Z, et al. Electronic Monitoring Systems for Hand Hygiene: Systematic Review of Technology. J Med Internet Res. 2021;23(11):e27880. DOI: 10.2196/27880
39. Sathitakorn O, Jantarathaneewat K, Weber DJ, Apisarnthanarak P, Rutjanawech S, Apisarnthanarak A. Efficacy of Environmental Cleaning Protocol Featuring Real-Time Feedback with and without PX-UV in Reducing the Contamination of Gram-Negative Microorganisms on High-Touch Surfaces in Four Intensive Care Units in Thailand. Antibiotics (Basel). 2023;12(3):438. DOI: 10.3390/antibiotics12030438
40. Seewald NJ. Adaptive Interventions for a Dynamic and Responsive Public Health Approach. Am J Public Health. 2023;113(1):37-9. DOI: 10.2105/AJPH.2022.307187
41. Bhalla M, Aggarwal A, Fatima KH. Carbapenem-resistant bacteria on hand-

held and hands-free electronic devices of healthcare workers and non-healthcare workers in Delhi, India. Infect Prev Pract. 2021;3(3):100162. DOI: 10.1016/j.infpip.2021.100162

42. Khadse SN, Ugemuge S, Singh C. Impact of Antimicrobial Stewardship on Reducing Antimicrobial Resistance. Cureus. 2023;15(12):e49935. DOI: 10.7759/cureus.49935
43. Intensive Care Society. State of the Art (SOA) 2023 Congress Abstracts. J Intensive Care Soc. 2023;24(2 Suppl):1-196. DOI: 10.1177/17511437231183900
44. Junaid SB, Imam AA, Balogun AO, De Silva LC, Surakat YA, Kumar G, et al. Recent Advancements in Emerging Technologies for Healthcare Management Systems: A Survey. Healthcare (Basel). 2022;10(10):1940. DOI: 10.3390/healthcare10101940
45. Cornistein W, Santonato D, Novau PA, Fabbro LG, Jorge MF, Malvicini MA, et al. Synergy between infection control and antimicrobial stewardship programs to control carbapenem-resistant Enterobacterales. Antimicrob Steward Healthc Epidemiol. 2023;3(1):e162. DOI: 10.1017/ash.2023.437
46. Perez F, Villegas MV. The role of surveillance systems in confronting the global crisis of antibiotic-resistant bacteria. Curr Opin Infect Dis. 2015;28(4):375-83. DOI: 10.1097/QCO.0000000000000183
47. Lawal OP, Egwuatu EC, Akanbi KO, Orobator ET, Eweje OZ, Omotayo EO, et al. Fighting Resistance With Data: Leveraging Digital Surveillance to Address Antibiotic Misuse in Nigeria. Path Sci. 2025;11(3):1009-17. DOI: 10.22178/pos.96-3
48. Nazer LH, Zatarah R, Waldrip S, Ke JXC, Moukheiber M, Khanna AK, et al. Bias in artificial intelligence algorithms and recommendations for mitigation. PLOS Digit Health. 2023;2(6):e0000278. DOI: 10.1371/journal.pdig.0000278
49. Zuhair V, Babar A, Ali R, Oduoye MO, Noor Z, Chris K, et al. Exploring the Impact of Artificial Intelligence on Global Health and Enhancing Healthcare in Developing Nations. J Prim Care Community Health. 2024;15:21501319241245847. DOI: 10.1177/21501319241245847
50. Gong E, Wang H, Zhu W, Galea G, Xu J, Yan LL, et al. Bridging the digital divide to promote prevention and control of non-communicable diseases for all in China and beyond. BMJ. 2024;387:e076768. DOI: 10.1136/bmj-2023-076768
51. Fukami T. Enhancing Healthcare Accountability for Administrators: Fostering Transparency for Patient Safety and Quality Enhancement. Cureus. 2024;16(8):e66007. DOI: 10.7759/cureus.66007
52. Garcia R, Barnes S, Boukidjian R, Goss LK, Spencer M, Septimus EJ, et al. Recommendations for change in infection prevention programs and practice. Am J Infect Control. 2022;50(12):1281-95. DOI: 10.1016/j.ajic.2022.03.028
53. Shehab N, Alschuler L, McILvenna S, Gonzaga Z, Laing A, deRoode D, et al. The National Healthcare Safety Network's digital quality measures: CDC's automated measures for surveillance of patient safety. J Am Med Inform Assoc. 2024;31(5):1199-205. DOI: 10.1093/jamia/ocae038
54. Mader R, Damborg P, Amat JP, Bengtsson B, Bourély C, Broens EM, et al. Building the European Antimicrobial Resistance Surveillance network in veterinary medicine (EARS-Vet). Euro Surveill. 2021;26(4):2001359. DOI: 10.2807/1560-7917.ES.2021.26.4.2001359
55. Feng Y, Kristensen SR, Lorgelly P, Meacock R, Núñez-Elvira A, Rodés-Sánchez M, et al. Pay-for-Performance incentives for specialised services in England: a mixed methods evaluation. Eur J Health Econ. 2024;25(5):857-76. DOI: 10.1007/s10198-023-01626-2
56. Morency-Potvin P, Schwartz DN, Weinstein RA. Antimicrobial Stewardship: How the Microbiology Laboratory Can Right the Ship. Clin Microbiol Rev. 2017;30(1):381-407. DOI: 10.1128/CMR.00066-16
57. Subrahmanya SVG, Shetty DK, Patil V, Hameed BMZ, Paul R, Smriti K, et al. The role of data science in healthcare advancements: applications, benefits, and future prospects. Ir J

Med Sci. 2022;191(4):1473-83. DOI: 10.1007/s11845-021-02784-z

58. Branda F, Scarpa F. Implications of Artificial Intelligence in Addressing Antimicrobial Resistance: Innovations, Global Challenges, and Healthcare's Future. Antibiotics (Basel). 2024;13(6):502. DOI: 10.3390/antibiotics13060502
59. Li L, Back E, Lee S, Shipley R, Mapitse N, Elbe S, et al. Balancing Risks and Opportunities: Data-Empowered-Health Ecosystems. J Med Internet Res. 2025;27:e57237. DOI: 10.2196/57237
60. Uwishema O, Masunga DS, Naisikye KM, Bhanji FG, Rapheal AJ, Mbwana R, et al. Impacts of environmental and climatic changes on future infectious diseases. Int J Surg. 2023;109(2):167-70. DOI: 10.1097/JS9.0000000000000231
61. Łukasik M, Porębska A. Responsiveness and Adaptability of Healthcare Facilities in Emergency Scenarios: COVID-19 Experience. Int J Environ Res Public Health. 2022;19(2):675. DOI: 10.3390/ijerph19020675
62. Lawal O, Elechi K, Adekunle F, Farinde O, Kolapo T, Igbokwe C, et al. A Review on Artificial Intelligence and Point-of-Care Diagnostics to Combat Antimicrobial Resistance in Resource-Limited Healthcare Settings like Nigeria: Review Article. J Pharm Insights Res. 2025;3(2):166-75. DOI: 10.53011/jpir.2025.3.2.25
63. Lawal O, Oyebamiji HO, Kelenna IJ, Chioma FJ, Oyefeso E, Adeyemi BI, et al. A Review on Usage of Digital Health Literacy to Combat Antibiotic Misuse and Misinformation in Nigeria: Review Article. J Pharm Insights Res. 2025;3(2):258-69. DOI: 10.53011/jpir.2025.3.2.38

Australian Journal of Biomedical Research
(eISSN 3083-4708)

Review Article

Forecasting Physician Burnout Risk: The Role of Electronic Health Record (EHR) and Operational Data in Predictive Models of Burnout

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Received: Aug 15, 2025
Accepted: Aug 20, 2025

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Abstract:

Physician burnout is a persistent global concern, driven by workload pressures, administrative demands, and emotional strain. It undermines both physician well-being and patient care, making early detection and intervention critical. While numerous reviews have examined the prevalence and drivers of burnout, less attention has been given to predictive approaches using electronic health records (EHR) and operational data. This review addresses that gap by evaluating how such data have been incorporated into predictive models, highlighting both their utility and limitations. A narrative review was conducted using PubMed and Google Scholar to identify peer-reviewed studies published between 2014 and June 2025. Ten studies met the inclusion criteria. Findings show that EHR and operational data can capture important predictors of burnout—such as documentation time, after-hours charting, and administrative burden—and are valuable for identifying high-risk clinics. However, current models struggle to achieve accuracy at the individual level because they rely heavily on quantitative workload metrics while neglecting organizational culture, leadership support, and psychosocial factors. This review underscores the need for next-generation predictive models that integrate qualitative and contextual variables with EHR-based measures. By articulating this gap, our contribution lies in reframing EHR and operational data not as standalone predictors but as components of multi-faceted, context-aware models. For healthcare leaders and policymakers, this means investing in tools that combine clinical, organizational, and personal dimensions to better forecast burnout and inform targeted interventions.

Keywords: Physician burnout; Electronic Health Records (EHR); Operational data; Predictive models; Healthcare management.

Introduction

Physician burnout has emerged as a serious issue in the healthcare sector, garnering heightened focus because of its profound effects on healthcare professionals and the patients they care for. This work-related phenomenon is defined by a prolonged reaction to ongoing occupational stress, presenting itself through three main aspects: emotional exhaustion, depersonalization, and a diminished sense of personal achievement [1, 2]. The consequences of burnout extend significantly, impacting healthcare delivery by directly influencing both physicians and their work settings [3, 4]. Burnout results in diminished job performance, increased medical errors, lower patient satisfaction, and may even prompt early retirement or a reduction in clinical hours [5]. Professionals facing burnout frequently show reduced empathy and involvement with patients, potentially leading to adverse effects on patient safety and satisfaction [6]. The impact on healthcare providers, such as poor physical and emotional health and, in severe instances, suicidal ideation, highlights the need for monitoring and managing clinician burnout [7].

The prevalence of burnout among healthcare professionals has been on the rise. It was estimated that over half of all physicians-in-training and practicing physicians suffer from burnout [8-10]. 59.2% of anaesthesiologists in the United States reported high levels of burnout in 2020 [11]. In Rotenstein et al., (2018) review on the prevalence of burnout, it was found that emotional exhaustion and depersonalization were common, with burnout rates varying from 0% to over 80% in most of the studies reviewed [12]. A study conducted by Shaltout et al. (2023) involving 155 doctors found that 65.8% of them had burnout. Of which, 80%, 65.8%, and 80% experienced emotional exhaustion, depersonalization, and personal dissatisfaction, respectively [13]. There have also been reports of differences in the risk of burnout between male and female doctors, with female doctors being more likely to experience burnout than male doctors. This suggests that organizational and structural factors, such as administrative burden and work-life balance, play a role in the different levels of burnout [13,14].

As burnout becomes more prevalent, it is important to put in place better ways to prevent, forecast, and manage it. In this case, prediction models that incorporate operational and EHR data may be extremely advantageous in identifying doctors who are at risk of burnout early on so as to take immediate measures to address it. Adopting EHR data gives useful information about doctors' workloads, such as how much time they spend on paperwork, administration, and patient care, all of which can lead to burnout [15]. Using only EHR data to predict burnout does not give a full picture because it does not take into account other factors that can lead to burnout, like work-life balance, leadership support, and workplace culture. However, it does give some information about how much work physicians are exposed to [16]. Findings from studies show that adding operational data to EHR data could help better forecast which doctors are most likely to experience burnout. Young's (2025) study found that EHR-based models, when used with operational data like administrative conferencing and team cooperation, were very helpful in finding clinics with high burnout rates. The same study also found it hard to forecast burnout at the physician level, which shows that we need a better way to make predictions that incorporates both qualitative and quantitative data from the individual levels [15].

In line with this, machine learning (ML) models and algorithms have been gaining ground in predicting burnout; however, they lack clinical utility as they exhibit low sensitivity and specificity at the individual level of burnout predictions [15]. There are also issues concerning inconsistency in defining and measuring burnout across studies. For example, the Maslach Burnout Inventory (MBI), regarded as the gold standard for burnout assessment, is not universally adopted [17]. Therefore, there is a need for more comprehensive, multi-faceted models and holistic models that capture both individual and organizational factors impacting burnout, as well as standardized metrics that are reliable for burnout predictions [2].

Traditional approaches to assessing physician burnout have relied heavily on survey instruments such as the Maslach Burnout Inventory (MBI). While these tools are valuable for capturing self-reported experience, they are retrospective, time-intensive, and prone to response bias. In contrast, predictive models that leverage EHR and operational data offer a more objective, continuous, and scalable means of detecting risk. These data sources capture real-time workload indicators such as documentation time, after-hours charting, and communication burden, which can provide earlier and more actionable signals than periodic surveys. Thus, EHR- and operational data–driven models are particularly promising for advancing from descriptive prevalence studies toward proactive identification and intervention.

By exploring the application of EHR and operational data in the determination of physician burnout risk, this study seeks to address the gaps in current predictive models and offer possible measures

to embrace to ensure better prediction. Findings from this study inform healthcare management and policy on measures to improve patient care, increase physician well-being, and secure the long-term survival of healthcare institutions.

Methodology

In carrying out this review, a narrative review was adopted to investigate the impact of EHR and operational data in predicting physician burnout. A narrative review approach was selected rather than a systematic review because the field of predictive modeling for physician burnout is still relatively new and heterogeneous, with diverse methodologies, outcome measures, and limited comparable quantitative data. This format allowed for greater flexibility in synthesizing findings across different study designs and highlighting conceptual gaps, while a systematic review or meta-analysis would have been premature and potentially misleading given the variability of available evidence.

Literature search was conducted in PubMed and Google Scholar for peer-reviewed articles published from 2014 up to the search date (10th June, 2025). The search terms utilized were "physician burnout," "electronic health record," "EHR," "operational data," and "predictive models." The details of the combined search terms and search yield from each database are provided in Table 1. Suitable database filters were used. Within databases, titles and abstracts screening were handled, and manual deduplication was done for papers considered for inclusion. No duplicates were found. We selected original research studies on physician burnout in practice that used EHR or operational data to predict burnout and were published in English. We excluded articles without empirical data or predictive modelling. Narrative synthesis was carried out based on thematic analysis of the literature, facilitating a concentrated evaluation of forecasting strategies and principal findings in burnout research.

In addition to the eligibility criteria noted above, we excluded commentaries, opinion pieces, and reviews without empirical predictive modelling. Although formal meta-analysis was not feasible due to heterogeneity across studies, we undertook a basic appraisal of methodological rigor by noting study design, sample size, data sources, and clarity of burnout measurement. This descriptive assessment allowed us to weigh the strength of evidence when synthesizing findings, even though no formal risk-of-bias tool was applied, given the narrative scope of this review.

Table 1: Search Strategy

Database	Search Term	Search yield	Filters applied	Yield after filtering
PubMed	((Physician burnout[Title/Abstract]) OR (Burnout[Title/Abstract])) AND ((Electronic Health Record[Title/Abstract]) OR (EHR[Title/Abstract]))	371	Free full text, Comparative Study, Multicenter Study, Observational Study, Randomized Controlled Trial, 2014-2025	10
Google Scholar	((((Physician burnout[Title/Abstract]) OR (Burnout[Title/Abstract])) AND ((Electronic Health Record[Title/Abstract]) OR (EHR[Title/Abstract]))) AND (Operational data[Title/Abstract])) AND (Predictive models[Title/Abstract])	150	2014-2025	147

Results

Across studies, EHR and operational metrics consistently predicted clinic-level burnout patterns, but had limited precision for individual physicians. This limitation was reflected in several models regardless of design, suggesting the need for broader contextual data.

Literature Search and Study Characteristics

Figure 1 provides an overview of the search results and selection process that led to the final inclusion of ten studies that were included in this review.

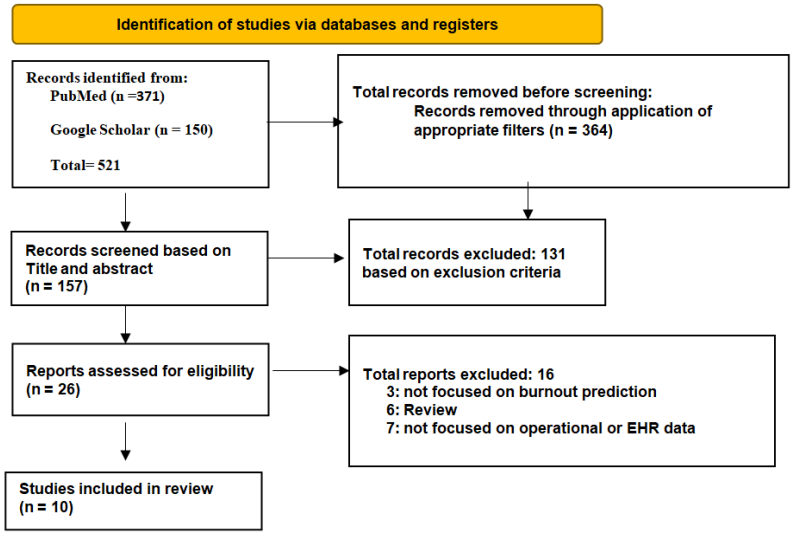
Identification of studies via databases and registers
Records identified from:
PubMed (n =371)
Google Scholar (n = 150)
Total= 521
Total records removed before screening:
Records removed through application of appropriate filters (n = 364)
Records screened based on Title and abstract (n = 157)
Total records excluded: 131 based on exclusion criteria
Reports assessed for eligibility (n = 26)
Total reports excluded: 16
3: not focused on burnout prediction
6: Review
7: not focused on operational or EHR data
Studies included in review (n = 10)

Figure 1: Prisma Flow Chart

The characteristics and overview of the 10 studies that fulfilled the inclusion criteria for this narrative review are detailed in Table 2. The studies utilized a range of methodologies, and the results are especially significant for comprehending predictive models related to physician burnout through the analysis of EHR and operational data.

Table 2: Characteristics and Summary of the included Studies

Serial Number	Study	Research Method	Key Findings	Source (Journal)	DOI
1	Hilliard et al., (2020) [18]	Cross-sectional study	Investigated EHR usage and its relation to burnout. Found strong correlations between administrative burdens and burnout.	Journal of Medical Informatics	http://doi.org/10.1093/jamia/ocaa092
2	Marmor et al. (2018) [19]	Longitudinal study	Evaluated burnout predictors, including EHR and workload. Found a significant link between EHR use and emotional exhaustion.	Applied clinical informatics	http://dx.doi.org/10.1055/s-0037-1620263

3	Linzer et al., (2016) [20]	Mixed-methods approach	Identified key EHR-related stressors leading to burnout. Found that EHR systems were linked to decreased personal accomplishment.	Journal of General Internal Medicine	https://doi.org/10.1007/s11606-016-3720-4
4	Cook et al., (2018) [21]	Cross-sectional study	Explored the role of EHR data in burnout prediction, showing high accuracy in burnout identification at the clinic level.	Journal of the American College of Cardiology	https://doi.org/10.1111/chd.12745
5	Kroth et al., (2019) [22]	Observational study	Investigated the impact of operational data on burnout. Found that operational inefficiencies contribute significantly to burnout.	JAMA Network Open	https://doi.org/10.1001/jamanetworkopen.2019.9609
6	Eschenroeder et al. (2021) [23]	Cross-sectional study	Analyzed EHR usage patterns and found a significant correlation with burnout levels. Also noted the impact of after-hours charting.	Journal of the American Medical Informatics Association	http://doi.org/10.1093/jamia/ocab053
7	McPeek-Hinz et al., (2021) [24]	Qualitative study	Discussed burnout prediction using EHR data. Found that predictive algorithms using EHR data showed limited precision but value at the clinic level.	JAMA Network Open	https://doi.org/10.1001/jamanetworkopen.2021.5686
8	Arndt et al., (2017) [25]	Cross-sectional study	Investigated burnout predictors in clinical settings. Found significant links between EHR administrative tasks and burnout risk.	Annals of Family Medicine	https://doi.org/10.1370/afm.2121
9	Sinsky et al. (2020) [26]	Observational study	Analyzed burnout about EHR usage and administrative burden. Found a strong correlation between EHR time and burnout severity.	Journal of the American Medical Informatics Association	https://doi.org/10.1093/jamia/ocz223
10	Shanafelt et al., (2022) [27]	Cross-sectional study	Focused on burnout prediction through EHR and operational data, finding that specific EHR features (e.g., documentation time) were predictive of burnout.	Mayo Clinic Proceedings	https://doi.org/10.1016/j.mayocp.2021.11.021

Narrative Synthesis

The narrative synthesis analyses the 10 research studies included for this evaluation, focusing on EHR and operational data in predicting physician burnout. The synthesis addresses predictive burnout modelling, EHR data integration, and model efficacy in healthcare. By critically examining the literature, we highlight progress in this field and identify gaps and possibilities to improve burnout prediction models.

Overview of Predictive Models for Physician Burnout

It is becoming more widely acknowledged that burnout among physicians is a significant problem that is impacting the healthcare system. As the rates of burnout keep increasing, particularly in high-stress situations such as emergency rooms, surgical departments, and intensive care units, predictive models are becoming increasingly important tools for identifying physicians who are at risk of burnout and putting early interventions into place [22]. In the included studies, the prediction models that were addressed focused on several aspects of burnout, such as emotional exhaustion, depersonalization, and decreased personal accomplishment, all of which are essential components of burnout [1].

Various kinds of data are utilised by these models; however, electronic health record (EHR) data in combination with operational data (such as workload and administrative stress) is becoming more recognized as a promising source for predicting burnout [24]. Research has shown that patterns of electronic health record (EHR) utilization, such as the amount of time spent on clinical documentation, working after hours, and the burden of communication (for example, through In-Basket messaging), are substantial predictors of the degree of burnout [26].

Role of EHR and Operational Data in Burnout Prediction Models

Combining operational data with electronic health records (EHR) is a key step in determining burnout rates and how to address the issue. From Electronic health record systems (EHR), objective and measurable data utilized in burnout prediction models can easily be derived [25]. Combining operational data and electronic health records (EHR) is a crucial part of the identification of physicians likely to experience burnout. These indicators show how much work doctors had to do, how much time they spent on clerical tasks, and how much patient data they had to deal with. Research like the one by Eschenroeder et al. (2021) shows that these operational data points give a full picture of the stress that doctors deal with every day [23].

It is worth noting that electronic health records are not only tools for passively collecting data. They also give information that can be acted on when combined with predictive algorithms. For example, McPeek-Hinz (2021) shows that EHR-based predictions have some problems when looking at burnout at individual levels, but they are useful for finding clinics with high burnout rates. This lets administrators focus their efforts where they are needed the most [24]. Linzer (2016) found that operational inefficiencies, which were revealed by measuring EHR use, are strongly linked to the likelihood of burnout. This result shows that fixing problems with the healthcare system could be the key to curtailing burnout [20].

Moreover, the fact that the data is so extensive and that burnout is extremely complex can make it hard for EHR-based algorithms to make accurate predictions [21]. These models look promising, but they rarely forecast accurately. This shows how important it is to have models that take into account other factors, like the organization's culture, support from leadership, and interpersonal relationships among healthcare professionals.

Comparative Analysis of Predictive Models

As various predictive models for burnout have emerged, the comparative analysis of these models is essential for identifying their strengths and weaknesses. Studies reviewed in this narrative synthesis indicate variability in the effectiveness of EHR-based models. Some models achieve high accuracy in predicting burnout at the clinic level, while others are more effective at predicting burnout symptoms at the individual level, as shown in Table 3 [21, 22].

Table 3 highlights several common themes across the predictive models, such as the significant role of EHR time, administrative burden, and operational metrics in predicting burnout. However, the models show limitations, particularly in their predictive accuracy at the individual level.

Table 3: Comparative Analysis of Predictive Models for Physician Burnout

Study	EHR Usage	Burnout Components Predicted	Model Type	Key Findings	Prediction Accuracy/Metric	Limitation
Hilliard et al., (2020) [18]	Time spent on documentation, messaging	Emotional exhaustion, depersonalization	Gradient Boosting	Strong correlation between documentation time and burnout symptoms.	AUC = 0.59	Limited predictive accuracy at the individual level
Marmor et al. (2018) [19]	EHR usage patterns, patient load	Emotional exhaustion, personal accomplishment	Logistic Regression	EHR usage correlates with emotional exhaustion and reduced personal accomplishment.	Sensitivity = 70%, Specificity = 85%	Excludes factors like organizational culture
Linzer et al., (2016) [20]	Time spent on EHR, administrative tasks	Emotional exhaustion, depersonalization	Random Forest	EHR and operational inefficiencies contribute significantly to burnout.	AUC = 0.65	Limited focus on organizational factors
Cook et al., (2018) [21]	Time on clinical notes, patient encounters	Emotional exhaustion, depersonalization	Hybrid Model	EHR data and operational factors combined for better predictions.	Sensitivity = 72%, Specificity = 78%	Needs inclusion of personal and organizational context
Kroth et al., (2019) [22]	EHR operational data, workload metrics	Emotional exhaustion, depersonalization	Decision Trees	Found strong links between operational inefficiencies and burnout.	AUC = 0.62	Does not account for interpersonal relationships
Eschenroeder et al. (2021) [23]	After-hours work, messaging	Emotional exhaustion, depersonalization	Machine Learning	Operational data identified burnout risk at the clinic level.	Sensitivity = 60%, Specificity = 85%	Limited prediction for individual burnout
McPeek-Hinz et al., (2021) [24]	EHR administrative burden	Emotional exhaustion	Predictive Algorithm	Identified clinics with high burnout rates through EHR metrics.	Sensitivity = 56%, Specificity = 85%	Inadequate precision for individual physicians

Arndt et al., (2017) [25]	Time spent on EHR, administrative messaging	Emotional exhaustion, depersonalization	Regression Model	EHR time is linked to increased burnout risk, especially in administrative tasks.	AUC = 0.68	Does not consider leadership or team dynamics
Sinsky et al. (2020) [26]	Time on documentation, In-Basket messaging	Emotional exhaustion, depersonalization, and personal accomplishment	Machine Learning	Found that EHR usage correlates strongly with burnout symptoms.	AUC = 0.72	Lack of consideration for organizational support and culture
Shanafelt et al., (2022) [27]	Time spent on documentation, patient load	Emotional exhaustion, depersonalization	Machine Learning	EHR features, such as time on documentation, identified at-risk physicians.	AUC = 0.75	Does not include emotional and team-based factors in prediction

Key Insights and Implications for Healthcare Management and Policy

As shown in this study, it is very important for people who work in healthcare management and policy to take a broad view of the issue of physician burnout. Even though electronic health records (EHRs) and operational data might be useful in detecting early warning signs of burnout, it's crucial to realize that this data should not be considered in isolation. To deal with the root causes of burnout and offer effective solutions, it is important to use a holistic strategy that considers personal well-being, organizational culture, and environmental factors, as well as leadership support [25, 26].

Furthermore, integrating predictive models into healthcare systems is a great way to lower the number of people who experience burnout. When used correctly, predictive models can help with initiatives that improve work conditions, reduce administrative loads, and boost the health of doctors. Future research should focus on making these models better by adding more factors, making predictions more accurate, and coming up with interventions that work on both personal and organizational levels.

Nevertheless, findings from this review have a profound impact on healthcare management. Healthcare providers can use operational data and electronic health records (EHRs) in the identification of doctors who are at risk of burnout and take proactive steps to minimize burnout and improve the quality of service. Moreover, to help healthcare workers avoid burnout, authorities should focus on programs that make electronic health records (EHRs) easier to use, cut down on administrative labor, and create a supportive workplace.

Discussion

According to the narrative synthesis of this review, predictive models employing EHR and operational data are instrumental in the identification and management of physician burnout. Various models yield distinct predictions depending on the nature of the data used [28]. Operational variables such as documentation, team communication, and administrative tasks have been incorporated into various models; however, they seldom serve as reliable predictors of burnout risk [29]. This is in line with Shanafelt et al.'s (2022) study, which indicated that models for predicting burnout, particularly those utilizing EHR data, show promise but are constrained in effectiveness without incorporating contextual or individual factors [27]. Moreover, burnout arises from a complex interplay of human, organizational, and

environmental factors, as noted by McPeek-Hinz et al. (2021). Operational statistics might fail to encompass the intricate nature of physician burnout [24].

Similar to the findings of Arndt et al. (2017), this study emphasizes the significance of qualitative insights within prediction models. As such, burnout models concentrating solely on operational variables such as EHR usage might overlook significant elements like interpersonal pressures and organizational culture, potentially clarifying why some predictions fall short of accuracy. Conversely, Wilton et al. (2024) and Adler-Milstein et al. (2020) recommended the integration of EHR data with self-reported burnout assessments to enhance the comprehension of physician well-being [29, 30]. Eschenroeder et al. (2021) demonstrated that predictive modelling in healthcare systems proved to be highly effective in pinpointing high-risk clinics for system-level interventions, even in the context of low burnout risk prediction [23]. Consequently, models for predicting burnout have the potential to enhance overall systems, particularly in environments characterized by high administrative demands or ineffective workflows, which contribute to increased burnout [19].

This study highlights the limitations of current prediction models, particularly those that utilize EHR and operational data. The findings indicate that while these models can identify trends, they are insufficient. Predictive EHR and operational data rarely consider burnout-causing psychological and organizational aspects. This limitation becomes apparent when examining the prevalence of burnout across various studies. Linzer et al. (2016) report a burnout prevalence variability of 38%, while McPeek-Hinz et al. (2021) indicate a variability of 52%. This suggests a need for more nuanced and multidimensional models [20, 24].

Therefore, incorporating individual-level psychosocial variables, environmental factors, and indicators of organizational culture can enhance the predictive accuracy of these models in future studies. Tawfik et al. (2024), Wilton et al. (2024), and Gardner et al. (2019) demonstrated that integrating survey data, personal wearables, and AI enhances prediction models alongside EHR metrics. This integration would enhance the predictive capabilities of these models and tailor burnout therapies to better address individual and systemic issues [28, 29, 31].

However, for these models to be effective, they need to be seamlessly integrated into the routine practices of healthcare professionals. Predictive models enable healthcare management to identify physicians who may be at risk for burnout early on, allowing for timely intervention. Predictive models could be added to EHR systems to flag doctors at high risk of burnout based on documentation or after-hours work [22]. These will help alert administrators to provide targeted support, such as lowering administrative responsibilities or offering flexible work schedules. Machine learning models could also detect and anticipate department or clinic burnout tendencies, enabling administrators to prioritize interventions in high-risk regions [27]. Adding these predictive models to hospital quality improvement activities could create a systematic approach to burnout prevention, aligning burnout prevention with patient care and physician satisfaction [26]. These models should diagnose and inform real-time decisions to improve work-life balance, job satisfaction, and patient outcomes.

Ultimately, this study recommends that healthcare organizations invest in technologies that can collect and integrate operational and qualitative data. This might include creating EHR systems that collect more detailed data on physician workload, work-life balance, and emotional well-being. To decrease burnout, healthcare management strategies should emphasize system-level measures that reduce administrative burden, improve team support, and promote good organizational culture. Hilliard et al. (2020) and Linzer et al. (2016) studies demonstrated how structural adjustments can increase physician well-being and patient care [18, 20].

Looking ahead, artificial intelligence and machine learning approaches hold promise for advancing burnout prediction by integrating multimodal data streams. By combining EHR metrics with operational indicators, survey-based measures, wearable device outputs, and organizational factors, AI-driven models could achieve greater sensitivity and specificity at the individual level. These approaches also enable dynamic, real-time monitoring, moving beyond static risk assessment toward adaptive systems that can trigger timely interventions. However, realizing this potential will require careful attention to data privacy, interoperability, and transparency in algorithmic decision-making [29].

Conclusion

EHR and operational data are powerful tools for detecting systemic drivers of physician burnout, particularly administrative burden and documentation load. However, current models fall short in reliably predicting individual risk, underscoring the need to broaden beyond quantitative workload measures. Future research should integrate organizational culture, psychosocial variables, and physician-reported experiences, potentially through AI and machine learning approaches that leverage multimodal data. For healthcare leaders, this means moving from isolated EHR metrics toward comprehensive, context-aware prediction models that support early intervention, reduce administrative burdens, and foster physician well-being alongside patient care.

Acknowledgements

Author Contributions: Emmanuel Olabayo Fagbenle conceived the study, coordinated the project, gathered the data, and conducted the review. Oladotun Solomon also contributed to the methodology and data analysis. Joubin Zahiri Khameneh provided supervision, critical review and data preparation. Oluwatomisin E. Arokodare assisted with literature review and manuscript editing.

Competing Interests: All the authors declare that they have no conflict of interest.

Ethics approval and consent to participate: Not applicable.

Consent for publication: Not applicable.

Availability of data and material: All the resources consulted in the review are provided in the reference section.

Funding: No funding of any kind was receive.

References

1. Maslach C, Jackson SE, Leiter MP. Maslach Burnout Inventory™ Manual. 4th ed. Menlo Park: Mind Garden, Inc.; 2018. Available from: https://www.mindgarden.com/maslach-burnout-inventory-mbi/685-mbi-manual.html
2. Lee J. Introduction to burnout and well-being for anesthesiologists in South Korea: narrative and brief review. Anesth Pain Med. 2025;20(2):121. doi: 10.17085/apm.25244
3. Sanford J. U.S. physician burnout rates drop yet remain worryingly high, Stanford Medicine-led study finds. Stanford Medicine News Center. 2025 Apr 9. Available from: https://med.stanford.edu/news/all-news/2025/04/doctor-burnout-rates-what-they-mean.html
4. De Hert S. Burnout in healthcare workers: prevalence, impact and preventative strategies. Local Reg Anesth. 2020;13:171–83. doi: 10.2147/LRA.S240564
5. Patel RS, Bachu R, Adikey A, Malik M, Shah M. Factors related to physician burnout and its consequences: a review. Behav Sci (Basel). 2018;8(11):98. doi: 10.3390/bs8110098
6. Han S, Shanafelt TD, Sinsky CA, Awad KM, Dyrbye LN, Fiscus LC, et al. Estimating the attributable cost of physician burnout in the United States. Ann Intern Med. 2019;170(11):784–90. doi: 10.7326/M18-1422
7. Cox T, Ahmed KW. Pandemic-related stress and suicide risk among healthcare professionals during the pandemic. Baylor Univ Med Cent Proc. 2025 Apr 4;1–6. doi: 10.1080/08998280.2025.2489875
8. Castillo M. Almost half of doctors experience at least one symptom of burnout, study finds. CBS News. 2012 Aug 21. Available from: https://www.cbsnews.com/news/almost-half-of-doctors-experience-at-least-one-symptom-of-burnout-study-finds/
9. Chandawarkar A, Chaparro JD. Burnout in clinicians. Curr Probl Pediatr Adolesc Health Care. 2021;51(11):101104. doi: 10.1016/j.cppeds.2021.101104
10. Yates SW. Physician stress and burnout. Am J Med. 2020;133(2):160–4. doi: 10.1016/j.amjmed.2019.08.034
11. Afonso AM, Cadwell JB, Staffa SJ, Zurakowski D, Vinson AE. Burnout rate and risk factors among anesthesiologists in the United States. Anesthesiology. 2021;134(5):683–96. doi: 10.1097/ALN.0000000000003722

12. Rotenstein LS, Torre M, Ramos MA, Rosales RC, Guille C, Sen S, et al. Prevalence of burnout among physicians: a systematic review. JAMA. 2018;320(11):1131–50. doi: 10.1001/jama.2018.12777
13. Shaltout AE, Mohamed MA, Ibrahim NM, Eldahshan NA. Prevalence of Burnout Syndrome among Working Physicians in Family Health Centres and Units in Port Said Governorate. Asian J Med Health. 2023;21(9):25–43. doi: 10.9734/ajmah/2023/v21i9853
14. Yeluru H, Newton HL, Kapoor R. Physician burnout through the female lens: a silent crisis. Front Public Health. 2022;10:880061. doi: 10.3389/fpubh.2022.880061
15. Young K. EHR data fails to predict physician burnout, may flag high-risk clinics. Mayo Clin Proc. 2025. Available from: https://www.consultant360.com/exclusive/ehr-data-fails-predict-physician-burnout-may-flag-high-risk-clinics
16. Singh R, Volner K, Marlowe D. The impact of work environment on provider burnout in healthcare systems. In: StatPearls. Treasure Island (FL): StatPearls Publishing; 2023. Available from: https://www.ncbi.nlm.nih.gov/books/NBK538330/
17. Simancas-Pallares MA, Fortich Mesa N, González Martínez FD. Validity and internal consistency of the Maslach Burnout Inventory in dental students from Cartagena, Colombia. Rev Colomb Psiquiatr. 2017;46(2):103–9. doi: 10.1016/j.rcp.2016.02.003
18. Hilliard RW, Haskell J, Gardner RL. Are specific elements of electronic health record use associated with clinician burnout more than others? J Am Med Inform Assoc. 2020;27(9):1401–10. doi: 10.1093/jamia/ocaa092
19. Marmor RA, Clay B, Millen M, Savides TJ, Longhurst CA. The impact of physician EHR usage on patient satisfaction. Appl Clin Inform. 2018;9(01):011–4. doi: 10.1055/s-0037-1620263
20. Linzer M, Poplau S, Babbott S, Collins T, Guzman-Corrales L, Menk J, et al. Worklife and wellness in academic general internal medicine: results from a national survey. J Gen Intern Med. 2016;31(9):1004–10. doi: 10.1007/s11606-016-3720-4
21. Cook SC, Marckini DN, Parker JL, Samuel B. Electronic Health Record Associated Stress in Adult Congenital Clinics. J Am Coll Cardiol. 2018;71(11S):A611. doi: 10.1111/chd.12745
22. Kroth PJ, Morioka-Douglas N, Veres S, Babbott S, Poplau S, Qeadan F, et al. Association of electronic health record design and use factors with clinician stress and burnout. JAMA Netw Open. 2019;2(8):e199609. doi: 10.1001/jamanetworkopen.2019.9609
23. Eschenroeder HC, Manzione LC, Adler-Milstein J, Bice C, Cash R, Duda C, et al. Associations of physician burnout with organizational electronic health record support and after-hours charting. J Am Med Inform Assoc. 2021;28(5):960–6. doi: 10.1093/jamia/ocab053
24. McPeek-Hinz E, Boazak M, Sexton JB, Adair KC, West V, Goldstein BA, et al. Clinician burnout associated with sex, clinician type, work culture, and use of electronic health records. JAMA Netw Open. 2021;4(4):e215686. doi: 10.1001/jamanetworkopen.2021.5686
25. Arndt BG, Beasley JW, Watkinson MD, Temte JL, Tuan WJ, Sinsky CA, et al. Tethered to the EHR: primary care physician workload assessment using EHR event log data and time-motion observations. Ann Fam Med. 2017;15(5):419–26. doi: 10.1370/afm.2121
26. Sinsky CA, Rule A, Cohen G, Arndt BG, Shanafelt TD, Sharp CD, et al. Metrics for assessing physician activity using electronic health record log data. J Am Med Inform Assoc. 2020;27(4):639–43. doi: 10.1093/jamia/ocz223
27. Shanafelt TD, West CP, Sinsky C, Trockel M, Tutty M, Wang H, et al. Changes in burnout and satisfaction with work-life integration in physicians and the general US working population between 2011 and 2020. Mayo Clin Proc. 2022;97(3):491–506. doi: 10.1016/j.mayocp.2021.11.021
28. Tawfik D, Bayati M, Liu J, Nguyen L, Sinha A, Kannampallil T, et al. Predicting primary care physician burnout from electronic health

record use measures. Mayo Clin Proc. 2024;99(9):1411–21. doi: 10.1016/j.mayocp.2024.01.005

29. Wilton AR, Sheffield K, Wilkes Q, Chesak S, Pacyna J, Sharp R, et al. The Burnout Prediction Using Wearable aNd Artificial Intelligence (BROWNIE) study: a decentralized digital health protocol to predict burnout in registered nurses. BMC Nurs. 2024;23(1):114. doi: 10.1186/s12912-024-01711-8
30. Adler-Milstein J, Zhao W, Willard-Grace R, Knox M, Grumbach K. Electronic health records and burnout: time spent on the electronic health record after hours and message volume associated with exhaustion but not with cynicism among primary care clinicians. J Am Med Inform Assoc. 2020;27(4):531–8. doi: 10.1093/jamia/ocz220
31. Gardner RL, Cooper E, Haskell J, Harris DA, Poplau S, Kroth PJ, et al. Physician stress and burnout: the impact of health information technology. J Am Med Inform Assoc. 2019;26(2):106–14. doi: 10.1093/jamia/ocy145

Australian Journal of Biomedical Research
(eISSN 3083-4708)

Review Article

Advances in Drug Discovery: Navigating Challenges and Embracing Innovation

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Received: Aug 04, 2025
Accepted: Aug 21, 2025

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Abstract:
It takes ten to fifteen years for a compound to progress from its identification to regulatory approval as a drug. Drug discovery is complex and resource-intensive process in which more than 90% of compounds never make it from bench to bedside and eventually get rejected during the development process. Experimental drugs failures often occur due to poor target selection, inadequate preclinical models, unforeseen toxicity, lack of efficacy in human trials, and the complexity of disease mechanisms, which make it difficult to predict drug responses accurately. Additionally, drug discovery is slowed down by a lack of collaboration between academia and industry, limiting the timely exchange of knowledge and expertise. Artificial intelligence (AI) is becoming an important tool in drug discovery, offering new possibilities to overcome existing challenges. It can help researchers identify better drug targets, make the screening process more efficient, and optimize drug design, which could speed up development and improve success rates. However, use of AI is associated with certain drawbacks such as potential exacerbation of healthcare gaps, protection of sensitive patient data and a need for informed consent. This review aims to discuss key challenges that hinder drug development process and explore future directions to enhance the efficiency of drug discovery.

Keywords: Artificial intelligence; Disease mechanism; Drug discovery; Drug failure; Personalized medicine.

Introduction

The journey of a new drug from target identification to market approval takes ten to fifteen years, and depending on the therapeutic area, it might cost in the range of $314 million to $4.46 billion [1]. The developmental cost rises as the investigational agent progresses into the different stages, and it may fail to progress into the next stage for various reasons such as lack of clinical efficacy, toxicity or lack of funding. Despite the technological advances and rapid accumulation of knowledge, drug discovery is still somewhat stalling.

Even with significant time and financial resources invested, the overall success rate of developing a new drug from initial concept to regulatory approval is only 7.9% [2]. For instance, in the case of tuberculosis only two new drugs were approved by the Food and Drug Administration (FDA) over the last 50 years [3]. First-in-class drugs target novel biological pathways that have not been previously explored in clinical settings. There is high uncertainty about whether these targets will yield the desired therapeutic effect and high probability of observing off-target interactions. In contrast, modifying existing drugs involves well-characterized mechanisms, reducing the risk of unexpected failures [4]. A review of European drug approvals from 2000 to 2014 found that out of 1,345 newly approved medications, 51% were slightly modified versions of already existing chemical entities that did not offer improved therapeutic effect, and only 1% were considered innovations in therapeutic management [5]. Despite challenges, there was encouraging progress in some categories - between 2015 and 2021 FDA approvals of biological drugs increased with monoclonal antibodies (mAbs) being the most widely approved category [6].

Although a drug candidate may perform well and produce favorable outcomes during preclinical investigations, this success does not always translate into clinical efficacy or safety in humans. Oftentimes results of clinical studies may reveal new various limitations such as unforeseen side effects, reduction in efficacy and potential drug-drug interactions that were not apparent at the preclinical stage due to complexity of disease mechanisms in humans and below average predictive potential of studied animal models. Lack of collaboration between academia and industry may also be one of the factors contributing to delay in progress and scarcity of successful approvals as important information regarding new findings and regulatory measures does not reach in a timely manner or may get completely lost.

This review aims to explore the key obstacles in drug discovery, from scientific and technological limitations to financial and regulatory barriers, as well as new developments such as the emergent use of artificial intelligence (AI). By analyzing these challenges, we can gain insights into potential solutions that could reshape the future of pharmaceutical research and development.

Methodology

The literature used in this review was selected from peer-reviewed articles published between 2015 and 2020 from databases such as PubMed, Scopus and Google Scholar using search terms such as ‘drug discovery’, ‘pharmacological innovations’, ‘AI in drug development’, ‘challenges of drug discovery’. Papers were selected based on relevance to the theme, content quality and recency. No protocol of systematic review was used. Generative AI tools were not used in the preparation of this manuscript. Minor language editing tools were used to improve clarity and grammar.

Traditional drug discovery and it’s challenges

High Failure Rates

For pharmaceutical companies and academic institutions, progressing a drug candidate to Phase I clinical trials after extensive preclinical optimization is a significant accomplishment. However, the reality is that nine out of ten drug candidates that passed preclinical stages fail at some point during Phase I, II, or III of clinical trials and do not receive regulatory approval [7]. The percentage of failure during drug discovery is even higher than 90% if we consider the fact that many compounds do not make it past the preclinical stage. The large divide between preclinical and clinical research is oftentimes referred to as “the valley of death” [8].

While there are a number of reasons for drug failure during clinical trials, the primary reason at this stage appears to be due to inadequate efficacy. For example, a study of 640 phase III clinical trials by Huang et al. reported that out of the 344 (54%) failed trials 195 (57%) were due to lack of demonstrated efficacy, 59 (17%) failed due to safety concerns and 74

(22%) failed because of commercial reasons. Compounds developed by small and medium-sized companies were most likely to fail due to commercial reasons [9]. Interestingly, potentially effective drugs may also fail in demonstrating efficacy, due to several factors such as flaws in the design of the study, an unsuitable statistical endpoint, or performing an underpowered clinical trial where the number of patients is too small to be able to reject the null hypothesis [10]. In January 2025 navacaprant, a potential agent for treatment of major depressive disorder (MDD) failed to demonstrate statistically significant improvement on the primary endpoint compared to placebo [11].

Demonstrated efficacy also does not necessarily guarantee drug approval. For instance, Atabecestat is a β-secretase1 (BASE1) inhibitor that was intended to treat Alzheimer's disease that initially showed promising results such as a stable reduction in β-amyloid peptide (Aβ) levels, however it was discontinued due to reports of liver toxicity among patients [12]. Table 1 below shows more examples of drug candidates that failed during different stages of drug development in recent years [13-17]. The data was acquired from open access articles published between 2019 and 2025.

Table 1: Drug Candidate Failures at various development stages.

Drug name	Drug class	Year of failure	Drug discovery and development stage	Reason for failure
CNP520 (Umibecestat)	Inhibitor of the beta-site amyloid precursor protein cleaving enzyme-1	2019	Phase II-III clinical studies	Worsened cognitive decline in Alzheimer's patients [13]
Ziritaxestat	Small-molecule, selective autotaxin inhibitor	2021	Phase III clinical studies	Did not improve clinical outcomes compared with placebo in patients with idiopathic pulmonary fibrosis [14]
Lotiglipron	Small-molecule glucagon-like peptide-1 receptor agonist	2023	Phase II clinical trial	Indicated elevated liver enzymes, suggesting potential liver toxicity [15]
BIIB105	Antisense oligonucleotide for amyotrophic lateral sclerosis (ALS)	2024	Phase I-II clinical trial	Treatment did not result in a reduction in levels of plasma neurofilament light chain and had no impact on measures of function, breathing and strength [16]
Sozinibercept	*VEGF-C and VEGF-D inhibitor for* wet age-related macular degeneration	2025	Phase III clinical trials	*No difference observed in primary and secondary endpoints compared to standard of care [17]*

Complexity of disease mechanisms

Understanding the molecular mechanism of the target disease, its etiology and the compounds' mechanism of action are crucial for drug discovery. This will reduce the probability of failure in the more advanced stages of drug development and help in avoiding general toxicity, inappropriate drug target or interference of the host [3].

To understand the molecular mechanism of the disease, we must begin by examining the starting point and the condition's potential cause. The studies of disease etiology are complicated by the fact that a disease can be caused by a wide variety of factors such as genetic (higher susceptibility, inheritance, SNPs), epigenetic (methylation, miRNA), environmental (exposure to toxic substances, habits) and others such as age, pre-existing conditions, or nutrition [18]. These factors often act in combination and are closely linked

to how the disease progresses. However, studies of disease etiology and progression are complicated by the fact that the majority focus on researching the activity of a single or a limited number of biological molecules, but almost all disease processes involve a complex cascade of interactions between hundreds of chemical entities within the organism [19]. Genetic architecture of Alzheimer's disease involves 81 loci in the genome each of which individually may contribute to overall susceptibility to this disease [20].

The only preclinical systems that allow to observe progression of disease and the effect of the studied compound in a complex living organism are animal models. While some are more similar in normal and disease physiology to humans than others, such as pigs, their predictive capability is still far from ideal [21]. Animals models used most often in preclinical studies are represented by rodents and non-human primates [22]. Some of the factors contributing to complexity of disease mechanism are summarized on Figure 1.

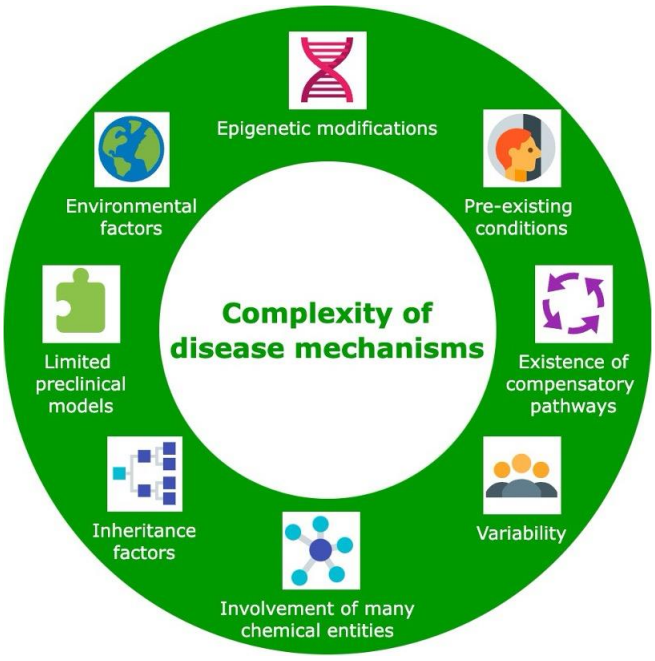

Figure 1: Complexity of disease mechanisms.

Interestingly, the FDA does not require elucidation of mechanism of action for a drug to be approved, and around 10-20% of the currently approved drugs do not have a known molecular target or certain mechanism of action [23]. For example, lithium used as first-line treatment of bipolar disorder does not have a clear mechanism that would explain its role in mood stabilization of patients despite having several unrelated theories and being effectively used for more than two centuries [24]. Even though some drugs may show clinical efficacy and be used despite a lack of knowledge about the way in which they exert their effect, understanding how they affect the drug target and off-target molecules could aid in the development of new generations of compounds with higher efficacy, lesser side effects and production costs.

Target Validation

The concept of target validation varies depending on the context but generally refers to the technical assessment of whether a target plays a crucial role in disease process and whether its pharmacological modulation could be effective in a specific patient population [25]. However, the process of target validation is complicated due to the fact that oftentimes there are fundamental differences between the course of disease in studied animal models and real humans [7]. A literature search of articles published from 2014 to 2024 revealed that the number of articles predicting potential drug-target interactions was increased, as well as the overall use of computational target identification and validation methods [26], however many of these computational predictions lack data regarding experimental validation.

Interestingly, there are a number of techniques available to assess the suitability of developmental agents targeting transcription factors and their protein interactions, something that was previously thought to be impossible. For instance, Nutlins (Nutley inhibitors), a class of compounds belong to cis-imidazoline analogs, found to serve as inhibitors of p53-MDM2 binding, which is p53 a known tumor suppressing protein largely controlled by MDM2. To validate whether nutlins actually inhibit the p53-MDM2 interaction and if so how, the crystal structure of MDM-Nutlin-2 complex was analyzed and inhibition was assessed using surface plasmon resonance technology [27].

One of the pitfalls of target validation observed, particularly in studies of new cancer treatments is the misinterpretation of correlative clinical data as causative, as two variables may be affected by an outside confounding factor and the association observed is due to chance [28]. For instance, an increase in expression of hypoxia-inducible factor (HIF) is associated with tumor growth, adaptation and poor prognosis for the patients [29]. However, this does not necessarily mean that HIF aids in tumor growth and increased malignancy, it could also indicate that as tumors increase in size their blood supply becomes insufficient and the increased expression of HIF is a response to these hypoxic conditions, or the observed association may be simply correlative [28]. Therefore, studying the nature of the relationship between a potential drug target and the observed effect is one of

the concerns that need to be addressed during the target validation process.

Toxicity and side effects

Failure of the drug due to safety concerns is the third reason for abandoning potentially viable compounds [9]. While finding and validating a drug target is an important step in drug discovery, researchers must think beyond the target-specific effects of the drug because safety issues and side effects usually arise due to off-target interactions [30]. Some compounds, despite their demonstrated efficacy, are not practical or safe to use in real life conditions because of their toxicity profiles and potential side effects. The failure of clinical drug development due to lack of efficacy does not necessarily mean the drug candidates are ineffective. More often, they fail to demonstrate sufficient efficacy in the disease-targeted organs at the maximum tolerable dose (MTD), which already causes toxicity in healthy organs [7]. While these drugs would work at higher doses, patients cannot tolerate the associated toxicity.

For instance, overexpression of endoplasmic reticulum oxidoreductin-1α (Ero1α) protein that is necessary for oxidative protein folding in the endoplasmic reticulum (ER) is associated with poor prognosis in many types of cancer such as lung cancer [31], gastric cancer [32], colorectal cancer [33] and pancreatic cancer [34]. EN460 is a small molecular inhibitor of Ero1α that works to prevent re-oxidation of Ero1α by competing with its FAD cofactor [35]. While EN460 demonstrates strong specificity for Ero1α, the drug's potency in vivo is quite low and resulted in various toxic effects due to nonspecific interactions with free thiols [35], making it an unsuitable target for clinical usage in real patients, despite being an effective inhibitor [36].

Determining off-target interactions of new drug entities may lead to accumulation of new data regarding the molecular mechanisms of the drug's side effects. For example, panobinostat is a histone deacetylase (HDAC) inhibitor that prevents binding of histones to certain regions of DNA and used for the treatment of multiple myeloma. However, hypothyroidism is one of the major reported side effects observed following drug administration. A method called thermal proteome profiling (TPP) was used for detection of four off-target proteins one of which was found to be phenylalanine hydroxylase (PAH) [37]. Interestingly, in vivo studies showed that panobinostat was bound to rat liver PAH during enzymatic assays, which resulted in the inhibition of PAH and a consequently decreased in tyrosine levels leading to a discovery possibly explaining the observed side effect of hypothyroidism [38]. Therefore, the use of TPP and enzymatic assays early on in the drug development process could help researchers gain a better understanding of the investigational drug's side effect before transitioning into animal toxicology studies [39].

Personalized Medicine and Variability

Although the same diagnosis may manifest with some differences among patients, treatments are usually administered according to a standard protocol that rarely considers such variability. Thus, personalized medicine, also referred to a precision medicine, aims to collect and analyze patients' data from genomics and proteomics for provision of more individualized treatment options and to be able to precisely predict drug responses [39]. Personalized medicine has the potential to revolutionize medical spheres, such as diagnosis and preventive care as well as to customized treatment and clinical research to each individual patient [40]. However, it has several challenges; for example, targeting of certain proteins as a personalized drug target, proved to be challenging to implement at a large scale for several reasons. First, the diverse and heterogenous nature of proteins allows them to exist in different proteoforms, meaning that the protein product of a single gene may result in many structural forms due to genetic variation, alternative splicing and post-translational modifications [41]. As structure and form of the protein are closely related to its function, there is a necessity to precisely identify the particular proteoforms that could be used as a suitable drug target for a particular disease model. Secondly, complications of drug delivery to the desired site may arise because of localization of proteins to certain cellular structures as well as differences of protein expression in tissues [39].

One of the recently developed concepts that could shape the future of precision medicine is digital twin – a digital model that offers a holistic view of individual's biological systems by integrating data from genomics, proteomics, data from wearable devices and reported from patients themselves [42]. However the use of digital twins is associated with challenges similar to those faced by artificial intelligence such as quality of data collection and interpretation, privacy and security concerns, and ethical considerations [43]. Li et al. (2025) suggest that personalized treatment may be developed by organizing factors pertaining to disease in a network and analyzing it in terms of changes observed in corresponding proteins [44]. Digital twin could be used for modeling organ or tissue-specific progression of the disease as well as how a patient will respond to therapy over time [45].

However, since a digital twin is a relatively new development, it does not yet have clearly articulated and comprehensive methodology.

In addition, development of patient-specific disease models requires the availability of large data banks on genomics and proteomics, as well as equal representation of genders and different ethnicities in clinical trials [21]. Because personalized medicine heavily depends on availability of sensitive patient data for analysis, it is important to ensure that such data is securely guarded to prevent any leaks and maintain trust and compliance [40]. Another challenge facing personalized medicine, is treatment cost, which needs to be considered when developing drugs for personalized medicine, as patients may be unable to afford treatment despite its efficacy. Nivolumab, an example of targeted therapy involving monoclonal antibodies (mAbs) in lung cancer treatment has shown efficacy exceeding 70%, however it is financially challenging to obtain for patients and healthcare systems due to its high cost [46].

Lack of Collaboration Between Disciplines

Due to the more publication-oriented nature of research in academia only a very small number of investigators actually get to partner and work collaboratively with industry representatives to proceed from bench research to clinical studies [47]. This leads to a formation of a large gap between the drug 'discovery' and 'development' stages.

For example, proprotein convertase subtilisin/kexin type 9 (PCSK9) is an enzyme that regulates the metabolism of cholesterol, and its activity is associated with higher levels of low-density lipoprotein (LDL) in blood plasma [48]. Analysis of papers published over the last twenty years on the discovery of PCSK9 and development of its inhibitors showed that 9286 scientists and 4203 institutions collaborated and contributed to the body of knowledge regarding this enzyme [49]. However, 40% of collaborations were within the same institution and out of the 60% that involved inter-institutional collaborations only 20% were with pharmaceutical companies [49].

Although new treatments may originate from academia or government research, they cannot be widely distributed without industry involvement. Notably, among around a hundred agencies that participated in the development of COVID-19 vaccine 85% were represented by the private industry [50]. Collaboration between industry and academia is necessary because academic researchers may face monetary restrictions that prevent them from advancing to further stages of drug development as well as lack expertise necessary to make the compound appealing to the industry [47]. Today more than ever collaboration in science is made easier by the existence of online communication. Qualified specialists all across the globe are able to work together to gather and analyze experimental data with relative ease.

Financial Constraints and Regulatory Challenges

Translational research aims to bridge the gap between basic scientific research and clinical practice [8]. Unlike basic research, translational research is more difficult and costly, because it requires testing in complex organisms like animals and humans. When a drug candidate successfully moves through the preclinical stages of development the risks associated with its failure decrease, however the cost of experiments rises exponentially. In academia, progress tends to be considerably slower compared to industry partly because of financial constraints. A substantial part of research financing from a grant is dedicated to purchasing consumable reagents and equipment as well as salaries for employees, leaving little for further continuation to clinical trials [47]. Due to differences in funding, structure, and priorities, projects that take years in academia can take months to complete in industry [51]. Small and medium-sized companies are more likely to discontinue studies of potentially viable compounds due to a lack of funding [9]. In the light of recent findings academic industry partnership (AIP) is becoming more of a necessity than an optional addition, if the goal is to speed up and enhance drug discovery efforts. Notably, gap funding programs such as translational research grants, proof of concept programs, startup accelerators and philanthropic venture funds help to recruit and secure more outside capital for development of new drug products [52]. An example of proof-of-concept gap funding program is The Translational Therapeutics Accelerator (TRxA), established in 2022 by the Critical Path Institute (C-Path), which designed to help bridge the "valley of death" in drug development. This global initiative provides academic researchers with the financial resources and strategic guidance necessary to advance new therapies from early-stage of discovery to patient care [52]. It also supports third-party validation of key research findings by recruiting outside organizations to reproduce the observed results.

Regulatory challenges in drug discovery arise due to strict requirements imposed by health authorities to ensure the safety, efficacy, and quality of new drugs. These challenges can delay the development, increase costs, and limit innovation. The length of a standard drug development procedure

being 12 to 15 years is in part due to the need to adhere to regulatory guidelines and the time necessary to review and correct the research documentation. Historically, it was shown that during emergency situations the length of drug development timeline can be shortened dramatically with the support of regulatory organizations. For example, the development of COVID-19 vaccines was sped up due to the declaration of an emergent infectious disease (EID); and the use of conditional marketing authorization (CMA) [53]. With the usual regulatory obstacles removed, the vaccine was developed in about eight months, whereas the median development time from clinical research initiation to obtaining marketing authorization is more than seven years for drugs approved by European Medicines Agency (EMA) between 2021 and 2022 [53].

Usually, academic researchers have lower understanding of the regulatory affairs and how to navigate them than their industry counterparts, which is one of the reasons why collaboration would have mutual benefits [52]. O'Dwyer et al. (2023) identified four main phases that university–industry collaborations go through: the embryonic phase, initiation, engagement, and the established phase [54]. In the embryonic phase academic researchers identify potential areas of interest that could lead to industry collaboration, during the initiation phase that happens after 2 – 3 years network members get to establish trust, share goals and communicate their strategies and needs. Third engagement phase (years 3-7) is characterized by sharing knowledge, experience and funds, whereas in the fourth established phase after year 8 is marked by first central results and growth in size [54]. Based on that study, it is evident that university-industry collaborations need time, resources and mutual understanding of common and individual goals. Figure 2 shows an example of collaboration network that involves several academic institutions, pharmaceutical companies and government organizations. Achievement of success in drug discovery heavily depends on the establishment of collaboration networks in which knowledge and resources are shared to reach a common goal.

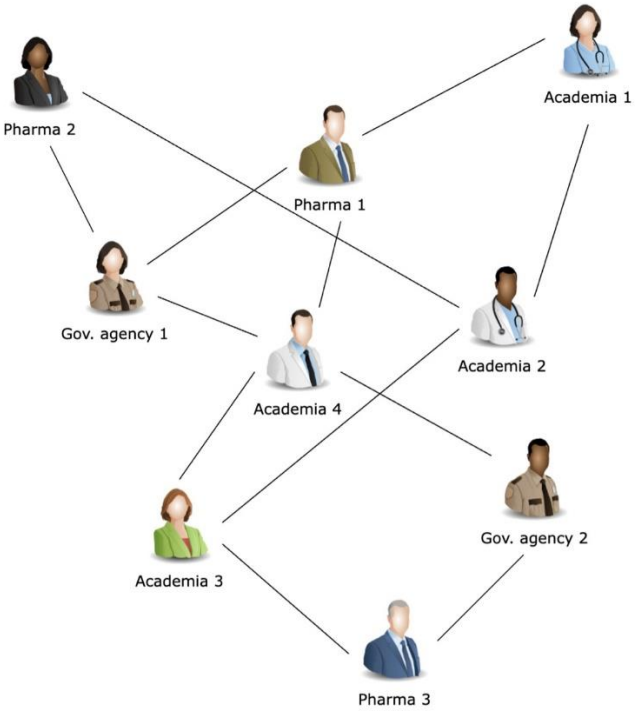

Figure 2: Collaboration between academia, government and industry.

Regulatory challenges in drug discovery require a balance between ensuring patient safety and promoting innovation. Special incentives exist to promote efforts of drug discovery by pharmaceutical companies, and they can largely be divided into push and pull incentives. Push incentives help sponsors by lowering research and development expenses, whereas pull incentives help by increasing profits from the market [55]. However, these incentives, it appears, have not led to sufficient investment for breakthrough drugs or solutions to unmet health needs, partly due to the fact that they primarily focus on the financial interest of pharmaceutical companies, which are not the only contributors to innovative health products [56].

Interventional Measures of the Challenges

Enhance Collaboration Efforts – Academia, Industry and Beyond

Pharmaceutical businesses aim to create practical and efficient solutions, conserve their value and maximize profits, whereas academic institutions are more likely to pursue high-risk and innovative endeavors [50], but this may actually be an advantage as illustrated by some cases of productive and mutually beneficial AIP. Prominent collaborations between the pharmaceutical industry and academia include partnerships such as AstraZeneca with Columbia University, Pfizer with the University of California at San Francisco, Monsanto with the University of Washington, and GlaxoSmithKline (GSK) with Harvard University, among others [57].

Similarly, the Wyss Institute for Biologically Inspired Engineering at Harvard University allowed for collaboration of faculty with industry professionals using the 'technology innovation funnel' model that gives academia an opportunity to develop creative ideas while refining and commercializing them with representatives from industry for a future real-life application [50].

Success of a partnership between academic institutions and pharmaceutical companies requires consideration of factors, such as acceptance of cultural differences and clear communication, despite potential differences in priorities regarding research, innovation and education [58]. Consistent communication and collaboration among research institutions, industry and sponsors is especially important during phase III clinical trials, due to a necessity to conduct large-scale studies that oftentimes span over multiple regions or continents and involve hundreds and thousands of participants [2].

Collaboration of large pharmaceutical corporations with artificial intelligence-driven drug discovery (AIDD) companies could also be beneficial in way that it allows for an exchange of computational models, proprietary datasets and finances [59].

Funding and Incentives

Clinical studies by academic researchers are much less supported by government organizations compared to basic science research, this is because translational efforts can be perceived as less favorable by some funding agencies . In a recent survey of academic researchers, with experiences in both academic clinical trials and industry-sponsored trials; found that academic trials have significantly less financial support at the time of their conduction compared to industry-sponsored trails [60]. Since grants provided by government organizations for academic research purposes are mostly insufficient to conduct clinical trials, academics have two ways in which they can conduct clinical trials: 1) by collaborating with industry partners, which can fulfill the monetary and regulatory knowledge gaps; 2) by participating in government-funded programs that support drug discovery efforts by academics.

However, existing push and pull incentives have failed to lead to sufficient investment for breakthrough drugs or solutions to unmet health needs. For instance, in the case of antibiotic development limitations such as restricted use and growing antibiotic resistance over time lead to insufficient market reward and despite their need and importance for the society as a whole antibiotic development is still stalling [61]. Additionally, despite the existence of incentives such as the Orphan Drug Act to encourage development of treatments for rare diseases challenges that discourage this pursuit such as limited knowledge of disease mechanism, low participation in clinical trials and flawed trial design still remain [62]. Since large companies are not the only contributors to biomedical progress, the current form of incentives needs to be revisited and modified to allow exchange of knowledge and involvement of more contributors, such as non-pharmaceutical firms to provide technological support and academic researchers to counter declining efficiency [56].

Innovations in Drug Discovery: Emergent Use of Artificial Intelligence

The introduction of artificial intelligence (AI) is revolutionizing many scientific spheres such as mathematics, chemistry, physics and medicine by making it easier to analyze large amounts of data in a relatively short timeframe. Traditional methodologies of drug discovery primarily rely on resource-intensive and prolonged experiments which have a high potential of yielding uncertain results [63]. Machine learning (ML) is a subset of AI that primarily serves to help learn patterns from data. Use of ML in drug discovery can significantly speed up and ease processes such as chemical synthesis, target validation, lead discovery, preclinical development and pharmacovigilance studies [64]. ML algorithms, through the analysis of extensive datasets, can uncover intricate patterns and trends that may not be immediately recognized by human scientists. This capability facilitates the discovery of novel bioactive compounds with reduced side effects at a significantly faster rate than classical protocols [63]. In 2020 with the help of AI based Centaur Chemist drug discovery platform Exscientia and Sumitomo Dainippon Pharma were able to develop DSP-118 a new drug candidate intended to treat obsessive-compulsive disorder (OCD) and it took 12 months to start phase I clinical trials, whereas traditional methods of drug discovery would require 4-5 years to reach phase I clinical trials [65]. DSP-118 is a first AI-designed compound and a potent, long-acting 5-HT1A receptor agonist [66]. A compound called ISM01-055, developed by Insilico Medicine to target the NCK-interacting protein kinase TNIK [67] for the treatment of idiopathic pulmonary fibrosis (IPF),

was one of the first AI-designed compounds to enter phase II clinical trials in June 2023 [68]. In a phase I clinical trial among 78 healthy participants ISM01-055 demonstrated comparable safety and pharmacokinetic profiles [67]. Xie et. al (2025) developed TransPharmer, a generative model which uses specific characteristic of pharmacophores, referred to as 'pharmacophore fingerprints' to synthesize new compounds with increased potency [69].

AI can help in generating predictive models for development of nanocarriers such as liposomes, micelles and nanoparticles by incorporating data on biological and physiochemical properties of the carriers and potential drug candidates [70]. The naïve Bayes algorithm can predict interactions of proteins and drugs and facilitate drug repurposing as a result [71]. Currently, deep learning techniques are also used to predict adverse drug reactions (ADRs) such as nausea, vomiting and diarrhea based on changes in gastrointestinal pacemaker activity (GIPA) using the Asian musk shrew (S. murinus) as model capable of vomiting [72].

However, AI is not a perfect and universal solution for drug discovery despite its potential advantages and its use is associated with certain challenges. Since ML heavily relies on availability of large and precise datasets; thus, if the studied data is limited or low in quality the resulting algorithms may become less accurate, less reproducible and less practical [73]. Another concern arises due to potential bias in data sets that may result in exacerbation of healthcare gaps between low-income and high-income countries [74]. Healthcare systems work with sensitive patient data such as medical histories, genetic profiles and other clinical documentation. Another disadvantage is that AI-based technologies can be susceptible to cyber threats and there is a growing need to develop strict security measures to protect sensitive patient data [75]. Furthermore, the application of patient data in training AI algorithms, raises ethical challenges related to informed consent and ownership of the data as patients may not completely understand how their data is being used, or may not have consented for its use in such manner [75]. Aside from data acquisition and safety concerns, there is also an issue of varying representation techniques – a single molecule may be represented by molecular graphs, molecular fingertips and SMILES (Simplified Molecular Input Line Entry System) [76], analyzing all these data together would require sophisticated algorithms as well as specialist capable of understanding the relationship between features of an input and corresponding output properties [77].

Conclusion

Identifying and developing new treatments is a long, complicated and expensive process that relies on extensive research and investment. In more than 90% of cases, chemical entities being studied as potential treatments for existing diseases never make it through the bench to bedside journey and those that do, are most likely modified versions of already existing compounds and may not offer additional health benefits. Current drug discovery efforts are limited due to lack of demonstrated efficacy, inadequate preclinical models, organ toxicity, complex mechanisms of action and financial constraints.

However, incentives and options for conditional authorization provided by regulatory agencies can markedly facilitate and speed up the development of new drugs. It is also evident that the success of drug discovery efforts in the future heavily depends on mutually beneficial collaboration between academic institutions and industry partners. Research collaboration of industry and academia consists of several stages, which may span over years or even decades. On one hand, such long-term collaboration efforts allow to transfer knowledge and innovation, sustain resources and funding in a stable and reliable manner. On the other hand, over time, the goals of academia and industry may diverge, leading to potential misalignments. Furthermore, potential disputes over intellectual property rights for innovative ideas may be one of the factors discouraging academic researchers from participating in such collaboration. Both academia and industry need to be incentivized, albeit for different purposes: the former to conduct clinical trials following the results from preclinical studies, and the latter to invest in developing therapies in areas perceived as less financially favorable.

Since their introduction, various computational methods have been increasingly utilized in drug discovery to automate and enhance the process. The emergent use of AI in drug development holds promise for a more accelerated, refined and precise process. Recent advancements, such as AI-designed molecules (e.g., ISM01-055) entering clinical trials, illustrate AI's growing credibility. However, it still faces many challenges in terms of data acquisition, analysis and safety. While the technology is being refined to provide

reliable outcomes, major challenges such as data storage, diversity and safety need to be addressed to ensure patients' trust and compliance. If integrated effectively, AI could dramatically reduce the timelines and costs of drug discovery. Importantly, it could also reveal potential pitfalls in drug activity and toxicity prior to transitioning to animal studies.

Acknowledgement

Disclosures: The author has no conflicts of interest to declare.

Ethics approval: This work did not involve human participations or animal.

Funding: The study did not receive external funding.

References

1. Sertkaya A, Beleche T, Jessup A, et al. Costs of Drug Development and Research and Development Intensity in the US, 2000-2018. JAMA Netw Open. 2024;7(5):e2415445. doi: 10.1001/jamanetworkopen.2024.15445.
2. Kim E, Yang J, Park S, et al. Factors Affecting Success of New Drug Clinical Trials. Ther Innov Regul Sci. 2023;57(5):737–50. doi: 10.1007/s43441-023-00509-1.
3. Yuan T, Werman JM, Sampson NS. The pursuit of mechanism of action: uncovering drug complexity in TB drug discovery. RSC Chem Biol. 2021;2(2):423–40. doi: 10.1039/D0CB00226G.
4. Gil C, Martinez A. Is drug repurposing really the future of drug discovery or is new innovation truly the way forward? Expert Opin Drug Discov. 2021;16(8):829–31. doi: 10.1080/17460441.2021.1912733.
5. Annett S. Pharmaceutical drug development: high drug prices and the hidden role of public funding. Biol Futur. 2021;72(2):129–38. doi: 10.1007/s42977-020-00025-5.
6. Martins AC, Oshiro MY, Albericio F, et al. Trends and Perspectives of Biological Drug Approvals by the FDA: A Review from 2015 to 2021. Biomedicines. 2022;10(9):2325. doi: 10.3390/biomedicines10092325.
7. Sun D, Gao W, Hu H, et al. Why 90% of clinical drug development fails and how to improve it? Acta Pharm Sin B. 2022;12(7):3049–62. doi: 10.1016/j.apsb.2022.02.002.
8. Seyhan AA. Lost in translation: the valley of death across preclinical and clinical divide – identification of problems and overcoming obstacles. Transl Med Commun. 2019;4(1):18. doi: 10.1186/s41231-019-0050-7.
9. Hwang TJ, Carpenter D, Lauffenburger JC, et al. Failure of Investigational Drugs in Late-Stage Clinical Development and Publication of Trial Results. JAMA Intern Med. 2016;176(12):1826. doi: 10.1001/jamainternmed.2016.6008.
10. Fogel DB. Factors associated with clinical trials that fail and opportunities for improving the likelihood of success: A review. Contemp Clin Trials Commun. 2018;11:156–64. doi: 10.1016/j.conctc.2018.08.001.
11. Neumora Therapeutics Reports Data from KOASTAL-1 Study of Navacaprant in Major Depressive Disorder [Internet]. [cited 2025 Feb 20]. Available from: https://www.neumoratx.com/news
12. Bazzari FH, Bazzari AH. BACE1 Inhibitors for Alzheimer's Disease: The Past, Present and Any Future? Molecules. 2022;27(24):8823. doi: 10.3390/molecules27248823.
13. Tariot PN, Riviere M, Salloway S, et al. Reversibility of cognitive worsening observed with BACE inhibitor umibecestat in the Alzheimer's Prevention Initiative (API) Generation Studies. Alzheimers Dement. 2024;20(11):7745–61. doi: 10.1002/alz.14237.
14. Maher TM, Ford P, Brown KK, et al. Ziritaxestat, a Novel Autotaxin Inhibitor, and Lung Function in Idiopathic Pulmonary Fibrosis: The ISABELA 1 and 2 Randomized Clinical Trials. JAMA. 2023;329(18):1567. doi: 10.1001/jama.2023.5355.
15. Amin NB, Frederich R, Tsamandouras N, et al. Evaluation of an oral small-molecule glucagon-like peptide-1 receptor agonist, lotiglipron, for type 2 diabetes and obesity: A dose-ranging, phase 2, randomized, placebo-controlled study. Diabetes Obes Metab. 2025;27(1):215–27. doi: 10.1111/dom.16005.
16. Biogen and Ionis announce topline Phase 1/2 study results [Internet]. [cited 2025 Feb 20]. Available

from: https://investors.biogen.com/news-releases
17. Opthea announces COAST Phase 3 trial topline results [Internet]. [cited 2025 Feb 20]. Available from: https://www.opthea.com/investor-centre/asx-announcements/
18. Schriml LM, Lichenstein R, Bisordi K, et al. Modeling the enigma of complex disease etiology. J Transl Med. 2023;21(1):148. doi: 10.1186/s12967-023-03987-x.
19. Bano I, Butt UD, Mohsan SAH. New challenges in drug discovery. In: Novel Platforms for Drug Delivery Applications. Elsevier; 2023. p. 619–43. doi: 10.1016/B978-0-323-91376-8.00021-5.
20. Andrews SJ, Renton AE, Fulton-Howard B, et al. The complex genetic architecture of Alzheimer's disease: novel insights and future directions. EBioMedicine. 2023;90:104511. doi: 10.1016/j.ebiom.2023.104511.
21. Loewa A, Feng JJ, Hedtrich S. Human disease models in drug development. Nat Rev Bioeng. 2023;1(8):545–59. doi: 10.1038/s44222-023-00063-3.
22. De Meyer A, Meuleman P. Preclinical animal models to evaluate therapeutic antiviral antibodies. Antiviral Res. 2024;225:105843. doi: 10.1016/j.antiviral.2024.105843.
23. Moffat JG, Vincent F, Lee JA, et al. Opportunities and challenges in phenotypic drug discovery: an industry perspective. Nat Rev Drug Discov. 2017;16(8):531–43. doi: 10.1038/nrd.2017.111.
24. Davis RL. Mechanism of Action and Target Identification: A Matter of Timing in Drug Discovery. iScience. 2020;23(9):101487. doi: 10.1016/j.isci.2020.101487.
25. Emmerich CH, Gamboa LM, Hofmann MCJ, et al. Improving target assessment in biomedical research: the GOT-IT recommendations. Nat Rev Drug Discov. 2021;20(1):64–81. doi: 10.1038/s41573-020-0087-3.
26. Tanoli Z, Schulman A, Aittokallio T. Validation guidelines for drug-target prediction methods. Expert Opin Drug Discov. 2025;20(1):31–45. doi: 10.1080/17460441.2024.2430955.
27. Moustaqil M, Gambin Y, Sierecki E. Biophysical Techniques for Target Validation and Drug Discovery in Transcription-Targeted Therapy. Int J Mol Sci. 2020;21(7):2301. doi: 10.3390/ijms21072301.
28. Kaelin WG. Common pitfalls in preclinical cancer target validation. Nat Rev Cancer. 2017;17(7):441–50. doi: 10.1038/nrc.2017.32.
29. Qannita RA, Alalami AI, Harb AA, et al. Targeting Hypoxia-Inducible Factor-1 (HIF-1) in Cancer: Emerging Therapeutic Strategies and Pathway Regulation. Pharmaceuticals. 2024;17(2):195. doi: 10.3390/ph17020195.
30. Weaver RJ, Valentin J-P. Today's Challenges to De-Risk and Predict Drug Safety in Human "Mind-the-Gap." Toxicol Sci. 2019;167(2):307–21. doi: 10.1093/toxsci/kfy270.
31. Liu L, Wang C, Li S, et al. ERO1L Is a Novel and Potential Biomarker in Lung Adenocarcinoma and Shapes the Immune-Suppressive Tumor Microenvironment. Front Immunol. 2021;12:677169. doi: 10.3389/fimmu.2021.677169.
32. Seol S-Y, Kim C, Lim JY, et al. Overexpression of Endoplasmic Reticulum Oxidoreductin 1-α (ERO1L) Is Associated with Poor Prognosis of Gastric Cancer. Cancer Res Treat. 2016;48(4):1196–209. doi: 10.4143/crt.2015.189.
33. Chen P, Chen Y, Sharma A, et al. Inhibition of ERO1L induces autophagy and apoptosis via endoplasmic reticulum stress in colorectal cancer. Cell Signal. 2025;127:111560. doi: 10.1016/j.cellsig.2024.111560.
34. Zhang J, Yang J, Lin C, et al. Endoplasmic Reticulum stress-dependent expression of ERO1L promotes aerobic glycolysis in Pancreatic Cancer. Theranostics. 2020;10(18):8400–14. doi: 10.7150/thno.45124.
35. Blais JD, Chin K-T, Zito E, et al. A Small Molecule Inhibitor of Endoplasmic Reticulum Oxidation 1 (ERO1) with Selectively Reversible Thiol Reactivity. J Biol Chem. 2010;285(27):20993–1003. doi: 10.1074/jbc.M110.126599.
36. Zhang Y, Li T, Zhang L, et al. Targeting the functional interplay between endoplasmic reticulum oxidoreductin-1α and protein disulfide isomerase suppresses the progression of cervical cancer. EBioMedicine. 2019;41:408–19. doi: 10.1016/j.ebiom.2019.02.041.
37. Becher I, Werner T, Doce C, et al. Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. Nat Chem Biol. 2016;12(11):908–10. doi: 10.1038/nchembio.2185.
38. Pognan F, Beilmann M, Boonen HCM, et al. The evolving role of investigative toxicology in the pharmaceutical industry. Nat Rev Drug Discov. 2023;22(4):317–35. doi: 10.1038/s41573-022-00633-x.
39. Su J, Yang L, Sun Z, et al. Personalized Drug Therapy: Innovative Concept Guided With

Proteoformics. Mol Cell Proteomics. 2024;23(5):100737. doi: 10.1016/j.mcpro.2024.100737.
40. Pandey A, Gupta SP. Personalized Medicine: A Comprehensive Review. Orient J Chem. 2024;40(4):933–44. doi: 10.13005/ojc/400403.
41. Forgrave LM, Wang M, Yang D, et al. Proteoforms and their expanding role in laboratory medicine. Pract Lab Med. 2022;28:e00260. doi: 10.1016/j.plabm.2021.e00260.
42. Vallée A. Envisioning the Future of Personalized Medicine: Role and Realities of Digital Twins. J Med Internet Res. 2024;26:e50204. doi: 10.2196/50204.
43. Katsoulakis E, Wang Q, Wu H, et al. Digital twins for health: a scoping review. NPJ Digit Med. 2024;7(1):77. doi: 10.1038/s41746-024-01073-0.
44. Li X, Loscalzo J, Mahmud AKMF, et al. Digital twins as global learning health and disease models for preventive and personalized medicine. Genome Med. 2025;17(1):11. doi: 10.1186/s13073-025-01435-7.
45. Cellina M, Cè M, Alì M, et al. Digital Twins: The New Frontier for Personalized Medicine? Appl Sci. 2023;13(13):7940. doi: 10.3390/app13137940.
46. S D, R K. A Review of the Regulatory Challenges of Personalized Medicine. Cureus [Internet]. 2024;16(5). doi: 10.7759/cureus.67891.
47. Saqib U, Demaree IS, Obukhov AG, et al. The fate of drug discovery in academia; dumping in the publication landfill? Oncotarget. 2024;15:31–4. doi: 10.18632/oncotarget.28552.
48. Shapiro MD, Tavori H, Fazio S. PCSK9: From Basic Science Discoveries to Clinical Trials. Circ Res. 2018;122(10):1420–38. doi: 10.1161/CIRCRESAHA.118.311227.
49. Cheng F, Ma Y, Uzzi B, et al. Importance of scientific collaboration in contemporary drug discovery and development: a detailed network analysis. BMC Biol. 2020;18(1):138. doi: 10.1186/s12915-020-00868-3.
50. Reddy SSK, Chao S. Academic Collaborations with Industry: Lessons for the Future. J Investig Med. 2020;68(8):1305–8. doi: 10.1136/jim-2020-001636.
51. Tanaka ML, Lopez O. Outlook on Industry-Academia-Government Collaborations Impacting Medical Device Innovation. J Eng Sci Med Diagn Ther. 2024;7(2):025001. doi: 10.1115/1.4063464.
52. Everts M, Drew M. Successfully navigating the valley of death: the importance of accelerators to support academic drug discovery and development. Expert Opin Drug Discov. 2024;19(3):253–8. doi: 10.1080/17460441.2023.2284824.
53. Möhrle JJ. How long does it take to develop a new drug? Lancet Reg Health Eur. 2024;43:100998. doi: 10.1016/j.lanepe.2024.100998.
54. O'Dwyer M, Filieri R, O'Malley L. Establishing successful university–industry collaborations: barriers and enablers deconstructed. J Technol Transf. 2023;48(3):900–31. doi: 10.1007/s10961-022-09932-2.
55. Cama J, Leszczynski R, Tang PK, et al. To Push or To Pull? In a Post-COVID World, Supporting and Incentivizing Antimicrobial Drug Development Must Become a Governmental Priority. ACS Infect Dis. 2021;7(8):2029–42. doi: 10.1021/acsinfecdis.0c00681.
56. Sullivan JA, Gold ER. Exploring regulatory flexibility to create novel incentives to optimize drug discovery. Front Med. 2024;11:1379966. doi: 10.3389/fmed.2024.1379966.
57. Kiriiri GK, Njogu PM, Mwangi AN. Exploring different approaches to improve the success of drug discovery and development projects: a review. Futur J Pharm Sci. 2020;6(1):27. doi: 10.1186/s43094-020-00047-9.
58. Pantanowitz L, Bui MM, Chauhan C, et al. Rules of engagement: Promoting academic-industry partnership in the era of digital pathology and artificial intelligence. Acad Pathol. 2022;9(1):100026. doi: 10.1016/j.acpath.2022.100026.
59. Kint S, Dolfsma W, Robinson D. Strategic partnerships for AI-driven drug discovery: The role of relational dynamics. Drug Discov Today. 2024;29(4):104242. doi: 10.1016/j.drudis.2024.104242.
60. Hoffmann J-M, Bauer A, Grossmann R. Academic vs. industry-sponsored trials: A global survey on differences, similarities, and future improvements. J Glob Health. 2024;14:04204. doi: 10.7189/jogh.14.04204.
61. Roope LSJ. The economic challenges of new drug development. J Control Release. 2022;345:275–7. doi: 10.1016/j.jconrel.2022.03.023.
62. Burton A, Castaño A, Bruno M, et al. Drug Discovery and Development in Rare Diseases: Taking a Closer Look at the Tafamidis Story.

Drug Des Devel Ther. 2021;15:1225–43. doi: 10.2147/DDDT.S289772.
63. Blanco-González A, Cabezón A, Seco-González A, et al. The Role of AI in Drug Discovery: Challenges, Opportunities, and Strategies. Pharmaceuticals. 2023;16(6):891. doi: 10.3390/ph16060891.
64. Dara S, Dhamercherla S, Jadav SS, et al. Machine Learning in Drug Discovery: A Review. Artif Intell Rev. 2022;55(3):1947–99. doi: 10.1007/s10462-021-10058-4.
65. Xu Y, Liu X, Cao X, et al. Artificial intelligence: A powerful paradigm for scientific research. Innovation. 2021;2(4):100179. doi: 10.1016/j.xinn.2021.100179.
66. Farghali H, Kutinová Canová N, Arora M. The potential applications of artificial intelligence in drug discovery and development. Physiol Res. 2021;70(Suppl4):S715–22. doi: 10.33549/physiolres.934765.
67. Ren F, Aliper A, Chen J, et al. A small-molecule TNIK inhibitor targets fibrosis in preclinical and clinical models. Nat Biotechnol. 2025;43(1):63–75. doi: 10.1038/s41587-024-02143-0.
68. Hasselgren C, Oprea TI. Artificial Intelligence for Drug Discovery: Are We There Yet? Annu Rev Pharmacol Toxicol. 2024;64(1):527–50. doi: 10.1146/annurev-pharmtox-040323-040828.
69. Xie W, Zhang J, Xie Q, et al. Accelerating discovery of bioactive ligands with pharmacophore-informed generative models. Nat Commun. 2025;16(1):2391. doi: 10.1038/s41467-025-56349-0.
70. Vidhya KS, Sultana A, M NK, et al. Artificial Intelligence's Impact on Drug Discovery and Development From Bench to Bedside. Cureus [Internet]. 2023;15(9). doi: 10.7759/cureus.47486.
71. Han R, Yoon H, Kim G, et al. Revolutionizing Medicinal Chemistry: The Application of Artificial Intelligence (AI) in Early Drug Discovery. Pharmaceuticals. 2023;16(9):1259. doi: 10.3390/ph16091259.
72. Chau HC, Liu JYH, Rudd JA. An application of deep learning model InceptionTime to predict nausea, vomiting, diarrhoea, and constipation using the gastro-intestinal pacemaker activity drug database (GIPADD). Sci Rep. 2025;15(1):13105. doi: 10.1038/s41598-025-95961-4.
73. Santa Maria JP, Wang Y, Camargo LM. Perspective on the challenges and opportunities of accelerating drug discovery with artificial intelligence. Front Bioinform. 2023;3:1121591. doi: 10.3389/fbinf.2023.1121591.
74. Nishan MNH. AI-powered drug discovery for neglected diseases: accelerating public health solutions in the developing world. J Glob Health. 2025;15:03002. doi: 10.7189/jogh.15.03002.
75. Boudi AL, Boudi M, Chan C, et al. Ethical Challenges of Artificial Intelligence in Medicine. Cureus [Internet]. 2024;16(7). doi: 10.7759/cureus.74495.
76. Qureshi R, Irfan M, Gondal TM, et al. AI in drug discovery and its clinical relevance. Heliyon. 2023;9(7):e17575. doi: 10.1016/j.heliyon.2023.e17575.
77. Marques A, Costa P, Velho S, et al. Analytical Techniques for Characterizing Tumor-Targeted Antibody-Functionalized Nanoparticles. Life. 2024;14(4):489. doi: 10.3390/life14040489.